



# SEQUENCE LISTING

<110> E. I. du Pont de Nemours and Company

<120> Lysophosphatidic Acid Acetyltransferases

<130> BB1332

<140> 09/914,098

<141> 2001-08-22

<150> 60/121,119

<151> 1999-02-22

<160> 58

<170> Microsoft Office 97

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<211> 928

<212> DNA

<213> Zea mays

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tcattggacca	cgcccaagca	cacgacctca	tcaggtattc	gttgcaaacc	atacatcgat	180
gatagatttc	attattctgg	agcaaatgac	agcatttgct	gtcatcatgc	agaagcatcc	240
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<213> Zea mays

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Pro	His	Gln	Val	Phe	Val	Ala	Asn	His	Thr	Ser	Met	Ile	Asp	Phe	Ile
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Ile	Leu	Glu	Gln	Met	Thr	Ala	Phe	Ala	Val	Ile	Met	Gln	Lys	His	Pro
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Gly	Trp	Val	Gly	Phe	Ile	Gln	Lys	Thr	Ile	Leu	Glu	Ser	Val	Gly	Cys
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Ile	Trp	Phe	Asn	Arg	Asn	Asp	Leu	Arg	Asp	Arg	Glu	Val	Thr	Ala	Arg
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Lys	Leu	Arg	Asp	His	Val	Gln	Gln	Pro	Asp	Asn	Asn	Pro	Leu	Leu	Ile
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Lys	Gly	Ala	Phe	Glu	Leu	Gly	Cys	Ala	Val	Cys	Pro	Ile	Ala	Ile	Lys
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Tyr	Asn	Lys	Ile	Phe	Val	Asp	Ala	Phe	Trp	Asn	Ser	Lys	Lys	Gln	Ser
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Phe	Thr	Met	His	Leu	Val	Arg	Leu	Met	Thr	Ser	Trp	Ala	Val	Val	Cys
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Asp	Val	Trp	Tyr	Leu	Pro	Pro	Gln	Tyr	Leu	Arg	Glu	Gly	Glu	Thr	Ala
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Ile	Ala	Phe	Ala	Glu	Arg	Val	Arg	Asp	Met	Ile	Ala	Ala	Arg	Ala	Gly
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Leu	Lys	Lys	Val	Pro	Trp	Asp	Gly	Tyr	Leu	Lys	His	Asn	Arg	Pro	Ser
225					230					235					240
Pro	Lys	His	Thr	Glu	Glu	Lys	Gln	Arg	Ile	Phe	Ala	Glu	Ser	Val	Leu
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aatcattact gaaaaagtaa ananatatac attatatttc ctcaaagcgc cgcaacacag 180
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tctctgcaaa ttcaatgggt gtctctctg gcttcaaatt ttgtggntcc aagtaccata 360
catcacannc nacagcccaa gatgtcatta attgcaagag atgnctgggt aangattgct 420
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      20              25              30

Trp Ala Val Xaa Cys Asp Val Trp Tyr Leu Xaa Pro Gln Asn Leu Lys
      35              40              45

Pro Gly Glu Thr Pro Ile Glu Phe Ala Glu Arg Val Arg Asp Ile Ile
      50              55              60

Ser His Arg Ala Gly Leu Lys Lys Val Pro Trp Asp Gly Tyr Xaa Lys
      65              70              75              80

Tyr Ser Arg Pro Ser Pro Lys His Arg Glu Gly Lys Gln Gln Ile Phe
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Xaa Glu Ser Val Leu Arg Arg Phe Glu Glu Lys
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 atttgctgtc atcatgcaaa agcatcctgg atggggttga tttattcaga agactattct 180  
 ggaaagtgtg gttgcatctg ggtttaaccg taatgatctc aaggatcgtg aagtagttgg 240  
 aagaaagtta cgtgatcaag ttcagcatcc agacaacaat cctctcttga ttttcccgga 300  
 aggaacttgt gttaataatc agtacactgt gatgttcaag aagggtgctt ttgagcttgg 360  
 ctgtgctgta tgtccaatag ctatcaaata taataaaata tttgttgacg ccttctggaa 420  
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 ctcttggtta gttgagggat ttccccttag ttgccttgta atctgttaat caccgaagt 780  
 agacctgggg catgtggaaa tgaccaccgc agttttgctg taaatttgtt tgcgggttga 840  
 cagaatcagt agcatgtgct tggcaagaaa gaactattga atcaaccttg ctatacatc 900  
 gacactagtc cgatttttgt acaccacaga tcaancgttg atccctgaac aaactgcagt 960  
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35 40 45  
Pro Gly Trp Val Gly Phe Ile Gln Lys Thr Ile Leu Glu Ser Val Val  
50 55 60  
Ala Ser Gly Phe Asn Arg Asn Asp Leu Lys Asp Arg Glu Val Val Gly  
65 70 75 80  
Arg Lys Leu Arg Asp Gln Val Gln His Pro Asp Asn Asn Pro Leu Leu  
85 90 95  
Ile Phe Pro Glu Gly Thr Cys Val Asn Asn Gln Tyr Thr Val Met Phe  
100 105 110  
Lys Lys Gly Ala Phe Glu Leu Gly Cys Ala Val Cys Pro Ile Ala Ile  
115 120 125  
Lys Tyr Asn Lys Ile Phe Val Asp Ala Phe Trp Asn Ser Lys Lys Gln  
130 135 140  
Ser Phe Thr Met His Leu Val Arg Leu Met Thr Ser Trp Ala Val Val  
145 150 155 160  
Cys Asp Val Trp Ser Trp Glu Pro Gln Tyr Leu Arg Glu Gly Glu Thr  
165 170 175  
Ala Ile Glu Phe Thr Glu Arg Val Arg Asp Met Ile Ala Ala Arg Ala  
180 185 190  
Gly Leu Lys Lys Val Pro Trp Asp Gly Tyr Leu Lys His Asn Arg Pro  
195 200 205  
Ser Pro Lys His Thr Glu Glu Lys Gln Arg Met Phe Ala Glu Ser Val  
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Leu Arg Arg Leu Glu Glu Asn  
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accaatttga agaatcccaa aggccagggg caattgtatc taatcatgtc tcttatgtgg 240  
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ggttgccact tattgggtctc ataagcaatt gtcttggtatg cattttttgtt caacgagaat 360  
cgaagtcttc agaagctaaa ggtgtctcag gcgctgtaac tgaaaggatc caagacgttt 420

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ttttgaaata cccttacagg agatttagtc cagcatggga ttcaatggat ggagcacgtc 600
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      20              25              30

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      35              40              45

Arg Arg Ser Thr Asn Ala Lys Gly Leu Asn Gln Asp Gln Phe Glu Glu
 50              55              60

Ser Gln Arg Pro Gly Ala Ile Val Ser Asn His Val Ser Tyr Val Asp
 65              70              75              80

Ile Leu Tyr His Met Ser Ala Ser Phe Pro Ser Phe Val Ala Lys Glu
      85              90              95

Ser Val Ser Arg Leu Pro Leu Ile Gly Leu Ile Ser Asn Cys Leu Gly
      100              105              110

Cys Ile Phe Val Gln Arg Glu Ser Lys Ser Ser Glu Ala Lys Gly Val
      115              120              125

Ser Gly Ala Val Thr Glu Arg Ile Gln Asp Val Cys Gln Asp Lys Asn
      130              135              140

Thr Pro Met Met Leu Leu Phe Pro Glu Gly Thr Thr Thr Asn Gly Asp
      145              150              155              160

Tyr Leu Leu Pro Phe Lys Thr Gly Ala Phe Leu Ala Gly Ala Pro Val
      165              170              175

Gln Pro Val Ile Leu Lys Tyr Pro Tyr Arg Arg Phe Ser Pro Ala Trp
      180              185              190

Asp Ser Met Asp Gly Ala Arg His Val Phe Leu Leu Leu Cys Gln Phe
      195              200              205

Val Asn His Met Glu Val Val Arg Leu Pro Val Tyr Tyr Pro Ser Gln
      210              215              220

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Leu Glu Lys Glu Asp Pro Lys Leu Tyr Ala Asn Asn Val Arg Lys Leu  
225 230 235 240

Ile Ala Met Glu Gly Asn Leu Val Leu Ser Asn Ile Gly Leu Ala Glu  
245 250 255

Lys Arg Val Tyr His Ala Ala Leu Thr Gly Ser Ser Leu Pro Gly Ala  
260 265 270

Arg His Glu Lys Asp Asp  
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tctctctctc tctctaaaac cctaattcta tacatggaag ggaaatctca aatctaataa 180  
ctaattaatt aatccatcga tcaagcatgg agtccgaact caaagacctc aattcgaagc 240  
cgccgaacgg caacggcaac agcggttcgag atgaccgtcc tctgctgaag ccggagcctc 300  
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20 25 30

Val Ser Ala Asp Ser Ile Ala Asp Met Glu Lys Lys Phe Ala Ala Tyr  
35 40 45

Val Arg Arg Asp Val Tyr Gly Thr Met Gly Arg Gly Glu Leu Pro Pro  
50 55 60

Lys	Glu	Lys	Leu	Leu	Leu	Gly	Phe	Ala	Leu	Val	Thr	Leu	Leu	Pro	Ile	65	70	75	80
Arg	Val	Val	Leu	Ala	Val	Thr	Ile	Leu	Leu	Phe	Tyr	Tyr	Leu	Ile	Cys		85	90	95
Arg	Val	Cys	Thr	Leu	Phe	Ser	Ala	Pro	Thr	Gly	Glu	Glu	Glu	Gln	Glu	100		105	110
Asp	Tyr	Ala	His	Met	Ser	Gly	Trp	Arg	Arg	Thr	Ile	Ile	Val	Ser	Cys	115		120	125
Gly	Arg	Ala	Leu	Ser	Arg	Leu	Met	Leu	Phe	Ile	Phe	Gly	Phe	Tyr	Trp	130		135	140
Ile	Pro	Glu	Ser	Asn	Ser	Ala	Ser	Gln	Glu	Asp	Lys	Ser	Arg	Gln	Pro	145	150	155	160
Glu	Glu	Leu	Arg	Arg	Pro	Gly	Val	Ile	Ile	Ser	Asn	His	Val	Ser	Tyr		165	170	175
Leu	Asp	Ile	Leu	Tyr	His	Met	Ser	Ser	Ser	Phe	Pro	Ser	Phe	Val	Ala		180	185	190
Lys	Arg	Ser	Val	Ala	Lys	Leu	Pro	Leu	Val	Gly	Leu	Ile	Ser	Lys	Cys	195		200	205
Leu	Gly	Cys	Val	Tyr	Val	Gln	Arg	Glu	Ser	Arg	Ser	Ser	Asp	Phe	Lys	210	215	220	
Gly	Val	Ser	Ala	Val	Val	Thr	Asp	Arg	Ile	Arg	Glu	Ala	His	Gln	Asn	225	230	235	240
Glu	Ser	Ala	Pro	Leu	Met	Met	Leu	Phe	Pro	Glu	Gly	Thr	Thr	Thr	Asn		245	250	255
Gly	Glu	Phe	Leu	Leu	Pro	Phe	Lys	Thr	Gly	Gly	Phe	Leu	Ala	Lys	Ala		260	265	270
Pro	Val	Leu	Pro	Val	Ile	Leu	Arg	Tyr	His	Tyr	Gln	Arg	Phe	Ser	Pro	275		280	285
Ala	Trp	Asp	Ser	Ile	Ser	Gly	Val	Arg	His	Val	Ile	Phe	Leu	Leu	Cys	290		295	300
Gln	Phe	Val	Asn	Tyr	Met	Glu	Val	Ile	Arg	Leu	Pro	Val	Tyr	His	Pro	305	310	315	320
Ser	Gln	Gln	Glu	Met	Asp	Asp	Pro	Lys	Leu	Tyr	Ala	Asn	Asn	Val	Arg		325	330	335
Arg	Leu	Met	Ala	Thr	Glu	Gly	Asn	Leu	Ile	Leu	Ser	Asp	Ile	Gly	Leu		340	345	350
Ala	Glu	Lys	Arg	Ile	Tyr	His	Ala	Ala	Leu	Asn	Gly	Asn	Asn	Ser	Leu	355		360	365
Pro	Ser	Val	Leu	His	Gln	Lys	Asp	Glu								370	375		

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 gtacctaaag atcactatga agaactggaa agaccagggg cgattgtatc taatcatgtg 180  
 tcatatgtgg acattcttta tcatatgtca gcttcttctc cgagttttgt tgctaagaac 240  
 tcagtgtcca agttgccgtt gattgggtctc ataagcaa atgtcttggtg catttttggt 300  
 caacgagaac caaatgttca gattctaaag ggtctcaagt gctgtaactg aaagtccatg 360  
 agntcacaag gacgagaatc cctatatcta ncctttcctg aggntacact acaatgggat 420  
 tactctccat tanacaganc ttcttgcan gacatgcaac tgtatttggn atacctacag 480  
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<220>  
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                     20                    25                    30  
 Arg Ser Phe Pro Asn Ala Glu Asp Val Pro Lys Asp His Tyr Glu Glu  
                     35                    40                    45  
 Leu Glu Arg Pro Gly Ala Ile Val Ser Asn His Val Ser Tyr Val Asp  
     50                    55                    60  
 Ile Leu Tyr His Met Ser Ala Ser Ser Pro Ser Phe Val Ala Lys Asn  
     65                    70                    75                    80  
 Ser Val Ser Lys Leu Pro Leu Ile Gly Leu Ile Ser Lys Cys Leu Gly  
                     85                    90                    95  
 Cys Ile Phe Val Gln Arg Glu Pro Asn Val Gln Ile Leu Lys Gly Leu  
                     100                    105                    110

Lys Cys Cys Asn Lys Ser Met Xaa Ser Gln Gly Arg Glu Ser Leu Tyr  
 115 120 125  
 Leu Xaa Phe Pro Glu Xaa Thr Leu Gln Trp Asp Tyr Ser Pro Leu Xaa  
 130 135 140  
 Arg Xaa Ser Cys Xaa Asp Met Gln Leu Tyr Leu Xaa Tyr Leu Gln Arg  
 145 150 155 160  
 Leu Ser Thr Trp Asp His Asp Gly Thr Gln Val Phe Ala Pro Xaa Phe  
 165 170 175  
 Xaa Xaa Xaa Arg Val Pro Ser Glu Xaa Leu Xaa Lys Arg Xaa Ser Ile  
 180 185 190

Ser Lys

<210> 13  
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 <212> DNA  
 <213> Arabidopsis thaliana

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 aaatcatgtt tcttatattg aaccaatctt ctacttctat gaattatcac cgaccattgt 180  
 tgcacggag tcacatgatt cacttccatt tgttggaact attatcaggg caatgcagg 240  
 gatatatgtg aatagattct cacagacatc aaggaagaat gctgtgcatg aaataaagag 300  
 aaaagcttcc tgcgatagat ttctctgctt gctgttatcc cccgaaggaa ccacgactaa 360  
 tgggaaagt cttatttctt tccaactcgg tgctttcatc cctgggttacc ctattcaacc 420  
 tgtagtagtc cggtatcccc atgtacattt tgatcaatcc tggggaaata tctctttgtt 480  
 gacgctcatg tttagaatgt tcaactcagtt tcacaatttc atggagggtg aatatcttcc 540  
 tgtaatctat cccagtgaag agcaaaagca gaatgctgtg cgtctctcac agaagactag 600  
 tcatgcaatt gcaacatctt tgaatgtcgt ccaaacatcc cattcttttg cggacttgat 660  
 gctactcaac aaagcaactg agttaaagct ggagaacccc tcaaattaca tgggtgaaat 720  
 ggcaagagtt gagtcgctat tccatgtaag cagcttagag gcaacgcgat ttttggatac 780  
 atttgtttcc atgattccgg actcgagtg gacgtgttagg ctacatgact ttcttcgggg 840  
 tcttaaaactg aaaccttgcc ctcttttctaa aaggatattt gagttcatcg atgtggagaa 900  
 ggtcggatca atcactttca aacagttctt gtttgccctg ggccacgtgt tgacacagcc 960  
 gctttttaag caaacatgcg agctagcctt tccccattgc gatgcagatg gagatggcta 1020  
 tattacaatt caagaactcg gagaagctct caaaaacaca atcccaaact tgaacaagga 1080  
 cgagattcga ggaatgtacc atttgctaga cgacgaccaa gatcaaagaa tcagccaaaa 1140  
 tgacttggtg tcttgcttaa gaagaaaccc tcttctcata gccatctttg cacctgactt 1200  
 ggccccaaca taacacagag agacaaaatg gctggctaag atttgtggtg cgatgattgt 1260  
 aaacttgtct ttgtgggtata ttattatacc ttttgttttg tcttcatatt tgatttcagc 1320  
 tagtaaaaag aagggaactgc tatgttttta gcctatatat ataccctcct ccaacatgga 1380  
 tccatccttt tgagtgttgg actataactg cttgtcgttt tccaccccaa aaaacgctat 1440  
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 a 1501

<210> 14  
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 <212> PRT  
 <213> Arabidopsis thaliana

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			20					25					30			
Glu	Ile	Ala	Pro	Ile	Val	Val	Ser	Asn	His	Val	Ser	Tyr	Ile	Glu	Pro	
		35					40					45				
Ile	Phe	Tyr	Phe	Tyr	Glu	Leu	Ser	Pro	Thr	Ile	Val	Ala	Ser	Glu	Ser	
	50					55					60					
His	Asp	Ser	Leu	Pro	Phe	Val	Gly	Thr	Ile	Ile	Arg	Ala	Met	Gln	Val	
65					70					75					80	
Ile	Tyr	Val	Asn	Arg	Phe	Ser	Gln	Thr	Ser	Arg	Lys	Asn	Ala	Val	His	
				85					90					95		
Glu	Ile	Lys	Arg	Lys	Ala	Ser	Cys	Asp	Arg	Phe	Pro	Arg	Leu	Leu	Leu	
			100					105					110			
Phe	Pro	Glu	Gly	Thr	Thr	Thr	Asn	Gly	Lys	Val	Leu	Ile	Ser	Phe	Gln	
		115					120					125				
Leu	Gly	Ala	Phe	Ile	Pro	Gly	Tyr	Pro	Ile	Gln	Pro	Val	Val	Val	Arg	
	130					135					140					
Tyr	Pro	His	Val	His	Phe	Asp	Gln	Ser	Trp	Gly	Asn	Ile	Ser	Leu	Leu	
145					150					155					160	
Thr	Leu	Met	Phe	Arg	Met	Phe	Thr	Gln	Phe	His	Asn	Phe	Met	Glu	Val	
				165					170					175		
Glu	Tyr	Leu	Pro	Val	Ile	Tyr	Pro	Ser	Glu	Lys	Gln	Lys	Gln	Asn	Ala	
			180					185					190			
Val	Arg	Leu	Ser	Gln	Lys	Thr	Ser	His	Ala	Ile	Ala	Thr	Ser	Leu	Asn	
		195					200					205				
Val	Val	Gln	Thr	Ser	His	Ser	Phe	Ala	Asp	Leu	Met	Leu	Leu	Asn	Lys	
	210					215					220					
Ala	Thr	Glu	Leu	Lys	Leu	Glu	Asn	Pro	Ser	Asn	Tyr	Met	Val	Glu	Met	
225					230					235					240	
Ala	Arg	Val	Glu	Ser	Leu	Phe	His	Val	Ser	Ser	Leu	Glu	Ala	Thr	Arg	
				245					250					255		
Phe	Leu	Asp	Thr	Phe	Val	Ser	Met	Ile	Pro	Asp	Ser	Ser	Gly	Arg	Val	
			260					265					270			
Arg	Leu	His	Asp	Phe	Leu	Arg	Gly	Leu	Lys	Leu	Lys	Pro	Cys	Pro	Leu	
		275					280					285				
Ser	Lys	Arg	Ile	Phe	Glu	Phe	Ile	Asp	Val	Glu	Lys	Val	Gly	Ser	Ile	
	290					295					300					
Thr	Phe	Lys	Gln	Phe	Leu	Phe	Ala	Ser	Gly	His	Val	Leu	Thr	Gln	Pro	
305					310					315					320	
Leu	Phe	Lys	Gln	Thr	Cys	Glu	Leu	Ala	Phe	Ser	His	Cys	Asp	Ala	Asp	
				325					330					335		

Gly Asp Gly Tyr Ile Thr Ile Gln Glu Leu Gly Glu Ala Leu Lys Asn  
340 345 350

Thr Ile Pro Asn Leu Asn Lys Asp Glu Ile Arg Gly Met Tyr His Leu  
355 360 365

Leu Asp Asp Asp Gln Asp Gln Arg Ile Ser Gln Asn Asp Leu Leu Ser  
370 375 380

Cys Leu Arg Arg Asn Pro Leu Leu Ile Ala Ile Phe Ala Pro Asp Leu  
385 390 395 400

Ala Pro Thr

<210> 15  
<211> 692  
<212> DNA  
<213> Oryza sativa

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gccacgcggg gcaccataac cacgacgacg acgacgagga gtcgccaacg gtgtgcggcg 180  
gcgatggcgg aggagggggg gacccgttcg cgttcctatc ggaggatcgg ccggcgtggt 240  
ggtcgccgcg gggggtgtcc ccggccgacc cgttcgcgaa cgggacgccg gggtggtgcg 300  
gggcgtacga gctcgtgagg gcgctcgtgt gcgcgcgggt ggcggcgggc aggctggtgc 360  
tgttcgggct ctccatcgcg gtgggggtacg ccgcccacgtg ggtggcgctc cgcgggtggg 420  
tcgacgtgcg ggagcggggc gcgcangagg gcgcggggcc catgccggcg tggcgccgcc 480  
gcctcatgtg gatcacgcgg attccgcgcg ctgcatactc ttctccttcg gatacatcgg 540  
ataaggagaa aggaaaaccg ccctagaaac ttactatnt ttctaaatca tgttcatcat 600  
agaaccatat actctcatag cttccgacat cgttctcaaa tccatatcat acattttgaa 660  
aatttcagca tcagtantag ttaaaatccc aa 692

<210> 16  
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<212> PRT  
<213> Oryza sativa

<220>  
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<222> (136)  
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20 25 30  
His Asn His Asp Asp Asp Asp Glu Glu Ser Pro Thr Val Cys Gly Gly  
35 40 45  
Asp Gly Gly Gly Gly Gly Asp Pro Phe Ala Phe Leu Ser Glu Asp Arg  
50 55 60  
Pro Ala Trp Trp Ser Pro Arg Gly Val Ser Pro Ala Asp Pro Phe Arg  
65 70 75 80  
Asn Gly Thr Pro Gly Trp Cys Gly Ala Tyr Glu Leu Val Arg Ala Leu  
85 90 95  
Val Cys Ala Pro Val Ala Ala Ala Arg Leu Val Leu Phe Gly Leu Ser  
100 105 110  
Ile Ala Val Gly Tyr Ala Ala Thr Trp Val Ala Leu Arg Gly Trp Val  
115 120 125  
Asp Val Arg Glu Arg Ala Ala Xaa Glu Gly Ala Gly Pro Met Pro Ala  
130 135 140  
Trp Arg Arg Arg Leu Met Trp Ile Thr Arg Ile Pro Arg Ala Ala Ser  
145 150 155 160  
Ser Ser Pro Ser Asp Thr Leu Asp Lys Glu Lys Gly Lys Pro  
165 170

<210> 17  
<211> 480  
<212> DNA  
<213> . Glycine max

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 cgctgcggct cgcgctgttc gggctctgcc tcgcggtggg gtacgtggcg acgaaggtgg 180  
 cgctggcang gtggnaggac aaggagaatc ccatgcccaa gtggaggtgt agggttatgt 240

ggatcacgcg cttgtgcgcc aaatgtattc tcttctcctt tggntatcan tggataaaac 300  
 ggnaagggaa acctgcacca aggggaaatt gctccaataa attgtatcta aaccatgttt 360  
 cntaanagtg agcctannct tcctatttct aagaattant tcctaacaat ggtgggaanc 420  
 tgaagncnca anactccata tccttttggt gggnaccaat taatagagca aatgnaagtc 480

<210> 18  
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 <212> PRT  
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<220>  
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<220>  
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 <222> (101)  
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 Ala Leu Cys Leu Pro Leu Ala Ala Leu Arg Leu Ala Leu Phe Gly Leu  
 35 40 45  
 Cys Leu Ala Val Gly Tyr Val Ala Thr Lys Val Ala Leu Ala Xaa Trp  
 50 55 60  
 Xaa Asp Lys Glu Asn Pro Met Pro Lys Trp Arg Cys Arg Val Met Trp  
 65 70 75 80  
 Ile Thr Arg Leu Cys Ala Lys Cys Ile Leu Phe Ser Phe Gly Tyr Xaa  
 85 90 95  
 Trp Ile Lys Arg Xaa Gly Lys Pro Ala Pro Arg  
 100 105

<210> 19  
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 <212> DNA  
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<222> (560)  
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 catctcggcc ccgcgagatt ggaagtgagg gcagggcagg gcggcagggg ccatggcggt 180  
 cccactcgtg ctcgctcgtgc tcccgctcgg cctcctcttc ctccctctccg gcctcaacgc 240  
 catccaggcc gtccctgtttc tctcgataag gccgttctcg aagagcttgt accggcggat 300  
 caacagggtc ttggccgagc tgctgtggct tcagctggtc tggcttgtgg attggtgggc 360  
 aggagttaag atacaactgc atgctgatga cgaaacttac aaggcaatgg ggaatgagca 420  
 tgcacttgtc atatcaaadc atcggagcga tatcgattgg cttattgggt ggattttggg 480  
 cacagcgtc aaggatgcct tgggaagtac acttgctgtt atgaagaaac atccgaaatc 540  
 cttccaatta ttgggctggn ccatgttgtt tgcagaatac cccttttttg gaaaaggact 600  
 gggcaaagga tgaaaagaca ttgaaatggg ggcccccaaa gggtgaanga cttccccaga 660  
 catttgggcn accctttttg tttaaggacc cccttaccca acaaaactcc aacaactcaa 720  
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 acac 784

<210> 20  
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 <212> PRT  
 <213> Oryza sativa

<220>  
 <221> UNSURE  
 <222> (130)  
 <223> Xaa = any amino acid

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 20 25 30  
 Arg Pro Phe Ser Lys Ser Leu Tyr Arg Arg Ile Asn Arg Phe Leu Ala  
 35 40 45

Glu	Leu	Leu	Trp	Leu	Gln	Leu	Val	Trp	Leu	Val	Asp	Trp	Trp	Ala	Gly
50						55					60				
Val	Lys	Ile	Gln	Leu	His	Ala	Asp	Asp	Glu	Thr	Tyr	Lys	Ala	Met	Gly
65					70					75					80
Asn	Glu	His	Ala	Leu	Val	Ile	Ser	Asn	His	Arg	Ser	Asp	Ile	Asp	Trp
				85					90					95	
Leu	Ile	Gly	Trp	Ile	Leu	Gly	Thr	Ala	Leu	Lys	Asp	Ala	Leu	Gly	Ser
		100						105					110		
Thr	Leu	Ala	Val	Met	Lys	Lys	His	Pro	Lys	Ser	Phe	Gln	Leu	Leu	Gly
		115					120					125			
Trp	Xaa	Met	Leu	Phe	Ala	Glu	Tyr	Pro	Phe	Leu	Gly	Lys	Gly	Leu	Gly
	130					135					140				

Lys Gly  
145

<210> 21  
 <211> 584  
 <212> DNA  
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 <222> (17)..(18)  
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ttgcagcagc ggccgtggtg gtaccattgg gcctgctctt cttegcctcc ggccctccttg 180
ttaatctcat tcaggcaata tgctatgtcg tcgtaaggcc ggtgtcgaaa agtttgtaca 240
gaaggatcaa ccgggtagta gcagagctct tgtggctgga gcttgtatgg cttattgatt 300
ggtgggcagg agttaaggtc caaatattca cagatcatga aacctttcgt ttaatgggta 360
aagagcatgc acttgtgata agcaatcaca gaagtatat tgattggctt gttggatggg 420
tttcagctca gcgttcagggt tgtcttggca gcactctaag ctgtgatgaa gaaatcttca 480
aagtttctgc cggtcattgg ctgggtcaatg tggttttcng agtaaccttt tctggagaag 540
aantnnggcc aaagatgaaa gccattaaa gtcangcatc ccgg 584

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<210> 22
<211> 116
<212> PRT
<213> Glycine max

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<400> 22
Met Ala Ile Ala Ala Ala Val Val Val Pro Leu Gly Leu Leu Phe
 1          5          10          15

Phe Ala Ser Gly Leu Leu Val Asn Leu Ile Gln Ala Ile Cys Tyr Val
          20          25          30

Val Val Arg Pro Val Ser Lys Ser Leu Tyr Arg Arg Ile Asn Arg Val
          35          40          45

Val Ala Glu Leu Leu Trp Leu Glu Leu Val Trp Leu Ile Asp Trp Trp
 50          55          60

Ala Gly Val Lys Val Gln Ile Phe Thr Asp His Glu Thr Phe Arg Leu
65          70          75          80

Met Gly Lys Glu His Ala Leu Val Ile Ser Asn His Arg Ser Asp Ile
          85          90          95

Asp Trp Leu Val Gly Trp Val Ser Ala Gln Arg Ser Gly Cys Leu Gly
          100          105          110

Ser Thr Leu Ser
          115

```

```

<210> 23
<211> 570
<212> DNA
<213> Triticum aestivum

```

```

<220>
<221> unsure
<222> (510)
<223> n = a, c, g, or t

```

```

<220>
<221> unsure
<222> (516)
<223> n = a, c, g, or t

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```

<220>
<221> unsure

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<222> (518)

<223> n = a, c, g, or t

<400> 23

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cctcctcttc ctctctccg gcctcgtcgt caacactgtc caggccgtat tggtcttgac 120
gataaggcca ttctcgaagc gattgtaccg gcagatcaac gtattcctgg ccgagttggt 180
gtggcttcag ctgatctggc ttgtggactg gtgggcaggt attaaggtag aggtgtatgc 240
ggatccagaa acttggaac taatgggcaa agagcacgcc cttctcatat ccaatcatcg 300
aagtgcatt gattggctgg ttggatggat tttagcacag cgttcaggat gtcttggaag 360
cgcaatagct ataatgaaga aatcctcaaa gttccttcca gttattgggt ggtccatgtg 420
gtttgcagaa tactcttttg gagagaactg gcaaaggatg aaaaacacta aatcgggtct 480
caaggtgaaa actccagata ttggctgccn tttgtnangg tcaaattact cacaaacttt 540
acagtaagaa atcatccaag ggttgcacgc 570
```

<210> 24

<211> 160

<212> PRT

<213> *Triticum aestivum*

<400> 24

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Met Ala Ile Pro Leu Val Leu Val Leu Leu Pro Leu Gly Leu Leu Phe
  1 5 10 15
```

```
Leu Leu Ser Gly Leu Val Val Asn Thr Val Gln Ala Val Leu Phe Leu
 20 25 30
```

```
Thr Ile Arg Pro Phe Ser Lys Arg Leu Tyr Arg Gln Ile Asn Val Phe
 35 40 45
```

```
Leu Ala Glu Leu Leu Trp Leu Gln Leu Ile Trp Leu Val Asp Trp Trp
 50 55 60
```

```
Ala Gly Ile Lys Val Gln Val Tyr Ala Asp Pro Glu Thr Trp Lys Leu
 65 70 75 80
```

```
Met Gly Lys Glu His Ala Leu Leu Ile Ser Asn His Arg Ser Asp Ile
 85 90 95
```

```
Asp Trp Leu Val Gly Trp Ile Leu Ala Gln Arg Ser Gly Cys Leu Gly
100 105 110
```

```
Ser Ala Ile Ala Ile Met Lys Lys Ser Ser Lys Phe Leu Pro Val Ile
115 120 125
```

```
Gly Trp Ser Met Trp Phe Ala Glu Tyr Ser Phe Gly Glu Asn Trp Gln
130 135 140
```

```
Arg Met Lys Asn Thr Lys Ser Gly Leu Lys Val Lys Thr Pro Asp Ile
145 150 155 160
```

<210> 25

<211> 1337

<212> DNA

<213> *Catalpa speciosa*

<400> 25

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gcacgagagg ctaaaggaca atgagcaagc taaaaacatc cagctccgaa ttggatttgg 60
atcaccccaa tatcgaagac tatcttccat ccgatccat tcaagagcct cacggcaagc 120
tccgcctgcg tgatttgctc gatatttcac caactctaac tgaggcagct ggtgccattg 180
```

```

ttgatgactc cttcacgaga tgcttcaagt caaatccgcc agaaccctgg aactggaaca 240
tatatttgtt tcctttgtgg tgcttaggag ttgttgtcag atatggtctt cttttccct 300
taagggtaat agtggtgaca ataggatgga ttatatcttct ctcatgctat ttccctgtgc 360
atttcctgtt aaaagggcat gacaaattga gaaaaaaatt agagagaggt ctagtggagt 420
tgatgtgcag tttttttgtt gcatcatgga ctgggggtgt caagtacat ggtccgcggc 480
ccagcatgcg gcctaagcag gtttttgtgg ctaatcacac atccatgatt gatttcattg 540
ttttggaaca aatgactgca tttgcagtga ttatgcagaa gcatcctggg tgggtaggac 600
tattgcagag cactattttg gagagtctag gatgtatctg gttcaaccgg tcagagtcca 660
aggaccgtga aattgttgca aaaaagctaa gagatcatgt ccatggcgct gataataatc 720
ctcttcttat attcccggaa ggaacatgtg tgaataacca ctacactgtg atgtttaaga 780
aggggtgcatt tgaacttgga tgcactgtct gtccaatcgc aatcaagtat aacaagattt 840
ttgtggatgc cttctggaac agcagaaagc aatcctttac aatgcacttg ttgcagctta 900
tgacatcctg ggctgttgtc tgtgatgttt ggtacctgga gcctcaaaat ctaaaacctg 960
gggaaacacc aattgaattt gctgagaggg tgagggggcat tatttctgtt cgagcaggcc 1020
ttaagaaggt gccgtgggat ggatatttga agtactctcg cccagccca aagcatcgtg 1080
agcgaagca acaaagcttc gcagagtcag ttctccatca cctggaagag aaatagattg 1140
aagataaata attttgttat ttactgtctt caatttggtt gatcaagttt gttagctgtt 1200
ttgaaattca atcttatttg tcactataaa gaggatttca gttcctcaat tgacataatg 1260
aaattccttt gatacgtcgt tgaagaggaa aatacaatat gaagtgttga aaaaaaaaaa 1320
aaaaaaaaaa aaaaaaa 1337

```

<210> 26  
 <211> 371  
 <212> PRT  
 <213> *Catalpa speciosa*

```

<400> 26
Met Ser Lys Leu Lys Thr Ser Ser Ser Glu Leu Asp Leu Asp His Pro
 1                5                10                15

Asn Ile Glu Asp Tyr Leu Pro Ser Gly Ser Ile Gln Glu Pro His Gly
      20                25                30

Lys Leu Arg Leu Arg Asp Leu Leu Asp Ile Ser Pro Thr Leu Thr Glu
      35                40                45

Ala Ala Gly Ala Ile Val Asp Asp Ser Phe Thr Arg Cys Phe Lys Ser
      50                55                60

Asn Pro Pro Glu Pro Trp Asn Trp Asn Ile Tyr Leu Phe Pro Leu Trp
      65                70                75                80

Cys Leu Gly Val Val Val Arg Tyr Gly Leu Leu Phe Pro Leu Arg Val
      85                90                95

Ile Val Leu Thr Ile Gly Trp Ile Ile Phe Leu Ser Cys Tyr Phe Pro
      100                105                110

Val His Phe Leu Leu Lys Gly His Asp Lys Leu Arg Lys Lys Leu Glu
      115                120                125

Arg Gly Leu Val Glu Leu Met Cys Ser Phe Phe Val Ala Ser Trp Thr
      130                135                140

Gly Val Val Lys Tyr His Gly Pro Arg Pro Ser Met Arg Pro Lys Gln
      145                150                155                160

Val Phe Val Ala Asn His Thr Ser Met Ile Asp Phe Ile Val Leu Glu
      165                170                175

```



Gln	Met	Thr	Ala	Phe	Ala	Val	Ile	Met	Gln	Lys	His	Pro	Gly	Trp	Val	
			180					185					190			
Gly	Leu	Leu	Gln	Ser	Thr	Ile	Leu	Glu	Ser	Leu	Gly	Cys	Ile	Trp	Phe	
		195					200					205				
Asn	Arg	Ser	Glu	Ser	Lys	Asp	Arg	Glu	Ile	Val	Ala	Lys	Lys	Leu	Arg	
	210					215					220					
Asp	His	Val	His	Gly	Ala	Asp	Asn	Asn	Pro	Leu	Leu	Ile	Phe	Pro	Glu	
225					230					235					240	
Gly	Thr	Cys	Val	Asn	Asn	His	Tyr	Thr	Val	Met	Phe	Lys	Lys	Gly	Ala	
				245					250					255		
Phe	Glu	Leu	Gly	Cys	Thr	Val	Cys	Pro	Ile	Ala	Ile	Lys	Tyr	Asn	Lys	
			260					265					270			
Ile	Phe	Val	Asp	Ala	Phe	Trp	Asn	Ser	Arg	Lys	Gln	Ser	Phe	Thr	Met	
		275					280					285				
His	Leu	Leu	Gln	Leu	Met	Thr	Ser	Trp	Ala	Val	Val	Cys	Asp	Val	Trp	
	290					295					300					
Tyr	Leu	Glu	Pro	Gln	Asn	Leu	Lys	Pro	Gly	Glu	Thr	Pro	Ile	Glu	Phe	
305					310					315					320	
Ala	Glu	Arg	Val	Arg	Gly	Ile	Ile	Ser	Val	Arg	Ala	Gly	Leu	Lys	Lys	
				325					330					335		
Val	Pro	Trp	Asp	Gly	Tyr	Leu	Lys	Tyr	Ser	Arg	Pro	Ser	Pro	Lys	His	
			340					345					350			
Arg	Glu	Arg	Lys	Gln	Gln	Ser	Phe	Ala	Glu	Ser	Val	Leu	His	His	Leu	
		355					360					365				
Glu	Glu	Lys														
		370														

<210> 27  
 <211> 1582  
 <212> DNA  
 <213> Zea mays

<400> 27  
 cctcgcccca tcgcggacct ttcctcggcg gcgtcgccat ctcatcggcg gcgggcgtgc 60  
 ggccggtggc cgaagccctt aggcgatggc gacctcgtct gtggcggcgg acatggagct 120  
 ggaccggcca aacctggagg actacctccc gcccgactcg ctcccgcagg aggcgccccg 180  
 gaatctccat ctgcgcgatc tgctggacat ctgcgcggtg ctcaccgagg cagcgggtgc 240  
 cattgtcgat gactccttca cacgggtgctt taagtcaaatt tctccagagc catggaattg 300  
 gaacatatat ctgttcccct tatgggtgctt tgggtgtagta ataagatatg gattactctt 360  
 cccactgagg tccttaacgc ttgcaatagg atggtttagca ttttttgctg ctttttttcc 420  
 tgtccatttc ctattgaaag gtcaagacaa gttgagaagt aaaattgaga ggaagttggt 480  
 tgaaatgatg tgcagtgttt ttgttgcttc atggactgga gttatcaagt atcatggacc 540  
 acgccaagc acacgacctc atcaggtatt cgttgcaaac catacatcga tgatagattt 600  
 cattattctg gagcaaatga cagcatttgc tgtcatcatg cagaagcatc ctggatgggt 660  
 tggatttatt cagaagacta tcttggaag tgtcggttgc atctggttta atcgtaatga 720  
 tctccgggac cgtgaagtta cggcacggaa gttacgtgat catgttcaac aaccagacaa 780  
 caatcctctg ttgatttttc cggaaggaac ttgtgtgaac aaccagtaca cggtcattgtt 840  
 caagaagggt gcctttgagc ttggctgcgc tgtatgtcca atagctatca agtacaataa 900

```

aatatttgtt gatgcctttt ggaacagtaa gaagcaatct ttacacatgc acttgggtccg 960
gctgatgaca tcatgggctg ttgtgtgtga tgtttggtac ttacctcctc aatatctgag 1020
ggagggagag acggcaattg catttgctga gagagtaagg gacatgatag ctgctagagc 1080
tggactaaag aaggttcctt gggatggcta tctgaaacac aaccgtccta gtcccaaaca 1140
cactgaagag aaacaacgca tatttgccga atctgtcttg atgagactgg aggagaaatg 1200
aagggacgta aagccgtaca agtgcacttc gttaggggtt tacatgcagc taccttgtaa 1260
ttcggttggc ttccagaaaa aaaaaagtga gcctgggaca cgtcaagtga ccacctcagt 1320
tttgttgtaa atttgttact agtttgatag gattattagt atgtacttat caggaaaaga 1380
attctcagta tgtgttttgg ctgcccattc aatgataggt cagtgattaa caccgaagca 1440
ttgtgctctc gtgagatgct gtgttggtct taatatattg acggtactgt accatgggtt 1500
aatgtgatt attgaagcaa tgtgaatgga ttagctggct aagaaaaaaa aaaaaaaaaa 1560
aaaaaaaaaa aaaaaaaaaa ag 1582

```

```

<210> 28
<211> 371
<212> PRT
<213> Zea mays

```

```

<400> 28
Met Ala Thr Ser Ser Val Ala Ala Asp Met Glu Leu Asp Arg Pro Asn
 1              5              10              15

Leu Glu Asp Tyr Leu Pro Pro Asp Ser Leu Pro Gln Glu Ala Pro Arg
      20              25              30

Asn Leu His Leu Arg Asp Leu Leu Asp Ile Ser Pro Val Leu Thr Glu
      35              40              45

Ala Ala Gly Ala Ile Val Asp Asp Ser Phe Thr Arg Cys Phe Lys Ser
      50              55              60

Asn Ser Pro Glu Pro Trp Asn Trp Asn Ile Tyr Leu Phe Pro Leu Trp
      65              70              75              80

Cys Phe Gly Val Val Ile Arg Tyr Gly Leu Leu Phe Pro Leu Arg Ser
      85              90              95

Leu Thr Leu Ala Ile Gly Trp Leu Ala Phe Phe Ala Ala Phe Phe Pro
      100             105             110

Val His Phe Leu Leu Lys Gly Gln Asp Lys Leu Arg Ser Lys Ile Glu
      115             120             125

Arg Lys Leu Val Glu Met Met Cys Ser Val Phe Val Ala Ser Trp Thr
      130             135             140

Gly Val Ile Lys Tyr His Gly Pro Arg Pro Ser Thr Arg Pro His Gln
      145             150             155             160

Val Phe Val Ala Asn His Thr Ser Met Ile Asp Phe Ile Ile Leu Glu
      165             170             175

Gln Met Thr Ala Phe Ala Val Ile Met Gln Lys His Pro Gly Trp Val
      180             185             190

Gly Phe Ile Gln Lys Thr Ile Leu Glu Ser Val Gly Cys Ile Trp Phe
      195             200             205

Asn Arg Asn Asp Leu Arg Asp Arg Glu Val Thr Ala Arg Lys Leu Arg
      210             215             220

```

Asp His Val Gln Gln Pro Asp Asn Asn Pro Leu Leu Ile Phe Pro Glu  
 225 230 235 240  
 Gly Thr Cys Val Asn Asn Gln Tyr Thr Val Met Phe Lys Lys Gly Ala  
 245 250 255  
 Phe Glu Leu Gly Cys Ala Val Cys Pro Ile Ala Ile Lys Tyr Asn Lys  
 260 265 270  
 Ile Phe Val Asp Ala Phe Trp Asn Ser Lys Lys Gln Ser Phe Thr Met  
 275 280 285  
 His Leu Val Arg Leu Met Thr Ser Trp Ala Val Val Cys Asp Val Trp  
 290 295 300  
 Tyr Leu Pro Pro Gln Tyr Leu Arg Glu Gly Glu Thr Ala Ile Ala Phe  
 305 310 315 320  
 Ala Glu Arg Val Arg Asp Met Ile Ala Ala Arg Ala Gly Leu Lys Lys  
 325 330 335  
 Val Pro Trp Asp Gly Tyr Leu Lys His Asn Arg Pro Ser Pro Lys His  
 340 345 350  
 Thr Glu Glu Lys Gln Arg Ile Phe Ala Glu Ser Val Leu Met Arg Leu  
 355 360 365  
 Glu Glu Lys  
 370

<210> 29  
 <211> 1422  
 <212> DNA  
 <213> Oryza sativa

<400> 29  
 gcacgagatc actgcgaaga tttcctcggc ggcggcggag gggatcgacg gaggggggga 60  
 tggcgacctc gtcggtggcg ggggacatcg agctggaccg gccgaacctg gaggactacc 120  
 tcccatccga ctcgctgccg caggagttcc ccaggaatct ccatctgcgc gatctgctgg 180  
 acatctcgcc ggtgctcact gaagcagcgg gcgccatcgt cgatgattca ttcacacggt 240  
 gctttaagtc aaattctcca gagccatgga attggaacat ttatttatcc ccattgtggt 300  
 gcttgggagt agtgataaga tacggaatac tattcccgtc gaggggccta actcttctag 360  
 ttggatgggt agcattcttt gctgcctttt ttctgtaca tttcttattg aaagggtcaaa 420  
 agatgagaag taaaatagag agaaagctgg ttgaaatgat gtgcagtgtt tttgttgctt 480  
 cttggactgg agtgatcaag tatcatgggc ctgcaccaag cacacggcct catcaggtat 540  
 ttgttgcaaa ccatacatcg atgatagatt tcattattct ggagcagatg acagcatttg 600  
 ctgtcattat gcaaaagcat cctggatggg ttggatttat tcagaagact atcttggaag 660  
 gtgttggttg catctgggtt aatcgcaatg atctcaagga tcgtgaagtg gttgcaaaaa 720  
 agttacgaga tcatgttcaa catccagaca gcaatcctct cctgattttc cctgaaggaa 780  
 cttgtgttaa caaccagtac actgtcatgt tcaagaaggg tgcttttgag cttggctgtg 840  
 ctgtatgccc aatagctatc aaatacaata aaatatattg tgatgccttc tggaatagta 900  
 agaagcaatc gtttacaatg cacttggtta ggcttatgac atcatgggca gttgtgtgtg 960  
 atgtatggta cttggagcct cagtatctga gggatggaga aacagcaatt gaatttgctg 1020  
 aaagagtaag agacatgata gctgctagag ctggtcttaa gaaggttccg tgggacgggt 1080  
 atctgaaaca caaccgccct agtcccaaac aactgaaga gaagcagcgc atctttgctg 1140  
 actctgtgtt gcggagactg gaggaagact aaacagatat caatcaactc tgggtgctcat 1200  
 tgggtgagtc aggttactaa tgtcctagtg tgtatctggg tctctggagt atgtggaaat 1260  
 taccactgca gttttgttgt aaattgtttg cagcttgaca gaatcaacat ttaatagcct 1320  
 gtattagcca agattttatg attgggttagg gttaacacat aaatattata ccttcccaaa 1380

tgatgtatta atacttaccc tcaaaaaaaaaa aaaaaaaaaa ac

1422

<210> 30

<211> 370

<212> PRT

<213> Oryza sativa

<400> 30

Met Ala Thr Ser Ser Val Ala Gly Asp Ile Glu Leu Asp Arg Pro Asn  
1 5 10 15

Leu Glu Asp Tyr Leu Pro Ser Asp Ser Leu Pro Gln Glu Phe Pro Arg  
20 25 30

Asn Leu His Leu Arg Asp Leu Leu Asp Ile Ser Pro Val Leu Thr Glu  
35 40 45

Ala Ala Gly Ala Ile Val Asp Asp Ser Phe Thr Arg Cys Phe Lys Ser  
50 55 60

Asn Ser Pro Glu Pro Trp Asn Trp Asn Ile Tyr Leu Phe Pro Leu Trp  
65 70 75 80

Cys Leu Gly Val Val Ile Arg Tyr Gly Ile Leu Phe Pro Leu Arg Gly  
85 90 95

Leu Thr Leu Leu Val Gly Trp Leu Ala Phe Phe Ala Ala Phe Phe Pro  
100 105 110

Val His Phe Leu Leu Lys Gly Gln Lys Met Arg Ser Lys Ile Glu Arg  
115 120 125

Lys Leu Val Glu Met Met Cys Ser Val Phe Val Ala Ser Trp Thr Gly  
130 135 140

Val Ile Lys Tyr His Gly Pro Arg Pro Ser Thr Arg Pro His Gln Val  
145 150 155 160

Phe Val Ala Asn His Thr Ser Met Ile Asp Phe Ile Ile Leu Glu Gln  
165 170 175

Met Thr Ala Phe Ala Val Ile Met Gln Lys His Pro Gly Trp Val Gly  
180 185 190

Phe Ile Gln Lys Thr Ile Leu Glu Ser Val Gly Cys Ile Trp Phe Asn  
195 200 205

Arg Asn Asp Leu Lys Asp Arg Glu Val Val Ala Lys Lys Leu Arg Asp  
210 215 220

His Val Gln His Pro Asp Ser Asn Pro Leu Leu Ile Phe Pro Glu Gly  
225 230 235 240

Thr Cys Val Asn Asn Gln Tyr Thr Val Met Phe Lys Lys Gly Ala Phe  
245 250 255

Glu Leu Gly Cys Ala Val Cys Pro Ile Ala Ile Lys Tyr Asn Lys Ile  
260 265 270

Phe Val Asp Ala Phe Trp Asn Ser Lys Lys Gln Ser Phe Thr Met His  
 275 280 285  
 Leu Val Arg Leu Met Thr Ser Trp Ala Val Val Cys Asp Val Trp Tyr  
 290 295 300  
 Leu Glu Pro Gln Tyr Leu Arg Asp Gly Glu Thr Ala Ile Glu Phe Ala  
 305 310 315 320  
 Glu Arg Val Arg Asp Met Ile Ala Ala Arg Ala Gly Leu Lys Lys Val  
 325 330 335  
 Pro Trp Asp Gly Tyr Leu Lys His Asn Arg Pro Ser Pro Lys His Thr  
 340 345 350  
 Glu Glu Lys Gln Arg Ile Phe Ala Asp Ser Val Leu Arg Arg Leu Glu  
 355 360 365  
 Glu Ser  
 370

<210> 31  
 <211> 1392  
 <212> DNA  
 <213> Sorghum

<400> 31  
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 gcagcgggtg ccatagtcga tgattcattc acgcgctgct ttaagtcgaa ttctccagaa 120  
 ccatggaact ggaacatata tttgttcctt ttatgggtgct tcggtgtagt aattcgatat 180  
 ggattactct tcccactgag gtccttaacg cttgcaatag gatggtttagc attttttgct 240  
 gcctttttcc ccgtgcattt cctattgaaa ggtcaagaca agttgagaaa taaaattgag 300  
 aggaagttgg ttgaaatgat gtgcagtgtt tttgttgctt catggactgg agtgatcaag 360  
 taccatggac cacgccaag cacacgacct catcaggat ttgttgcaaa ccatacatca 420  
 atgatagatt tcattattct ggagcaaatg acagcatttg ctgtcatcat gcagaagcat 480  
 cctggatggg ttggatttat tcagaagact atcttggaag gtgtgggttg catctgggtt 540  
 aaccgtaatg atctccggga tcgtgaagtt acggcacgga agttgcgtga tcatgttcaa 600  
 catccagaca aaaaccctct cttgattttc ccagaaggaa cttgtgttaa caaccagtat 660  
 acggtcatgt tcaagaaggg tgcctttgag cttgggtgtg ctgtctgtcc aatagctatc 720  
 aaatacaata aaatatattgt tgatgccttt tggaacagta agaagcaatc ttttacgatg 780  
 cacttggtcc gggtgatgac atcatgggct gttgtgtgtg atgtttggta cttggagcct 840  
 caatatctga gggagggaga gactgcaatt gcgtttgctg agagagtaag ggacatgata 900  
 gcagctagag ctggtcttaa gaaggtcccg tgggatggct atctgaaaca caaccgccct 960  
 agtcccaaac acaccgaaga gaagcaacgc atattcgccg aatctgtctt gaggagacta 1020  
 gaggagaaat gaagagacat caaacactac aagcgcattt ggtagtggt ttaccgttca 1080  
 gctaccttgt aattcggttg gctccccgaa aaaaaaaagt ccgggacacg tcaagtgcc 1140  
 agctcagttt tggtgtaaat ttattagaaa ttgacagaa ttggtagtgt gaacttacca 1200  
 agaaaggaag aatagccgca tgtgttggtg ctgttcattc tatgattggt taggaattga 1260  
 cacttgaaac acggtactct attcagaggc tgtgtccgta ttatgaatc gacgatgtaa 1320  
 tggttttaat tcatgtgatt attgattcaa taatatgagt agattaaaaa aaaaaaaaaa 1380  
 aaaaaaaaaa aa 1392

<210> 32  
 <211> 343  
 <212> PRT  
 <213> Sorghum

<400> 32  
 Ala Arg Ala Arg Asn Leu His Leu Arg Asp Leu Leu Asp Ile Ser Pro  
 1 5 10 15

Val	Leu	Thr	Glu	Ala	Ala	Gly	Ala	Ile	Val	Asp	Asp	Ser	Phe	Thr	Arg	
			20					25					30			
Cys	Phe	Lys	Ser	Asn	Ser	Pro	Glu	Pro	Trp	Asn	Trp	Asn	Ile	Tyr	Leu	
		35					40					45				
Phe	Pro	Leu	Trp	Cys	Phe	Gly	Val	Val	Ile	Arg	Tyr	Gly	Leu	Leu	Phe	
	50					55					60					
Pro	Leu	Arg	Ser	Leu	Thr	Leu	Ala	Ile	Gly	Trp	Leu	Ala	Phe	Phe	Ala	
	65				70					75					80	
Ala	Phe	Phe	Pro	Val	His	Phe	Leu	Leu	Lys	Gly	Gln	Asp	Lys	Leu	Arg	
				85					90					95		
Asn	Lys	Ile	Glu	Arg	Lys	Leu	Val	Glu	Met	Met	Cys	Ser	Val	Phe	Val	
			100					105					110			
Ala	Ser	Trp	Thr	Gly	Val	Ile	Lys	Tyr	His	Gly	Pro	Arg	Pro	Ser	Thr	
		115					120					125				
Arg	Pro	His	Gln	Val	Phe	Val	Ala	Asn	His	Thr	Ser	Met	Ile	Asp	Phe	
	130					135					140					
Ile	Ile	Leu	Glu	Gln	Met	Thr	Ala	Phe	Ala	Val	Ile	Met	Gln	Lys	His	
145					150					155					160	
Pro	Gly	Trp	Val	Gly	Phe	Ile	Gln	Lys	Thr	Ile	Leu	Glu	Ser	Val	Gly	
				165					170					175		
Cys	Ile	Trp	Phe	Asn	Arg	Asn	Asp	Leu	Arg	Asp	Arg	Glu	Val	Thr	Ala	
			180					185					190			
Arg	Lys	Leu	Arg	Asp	His	Val	Gln	His	Pro	Asp	Lys	Asn	Pro	Leu	Leu	
		195					200					205				
Ile	Phe	Pro	Glu	Gly	Thr	Cys	Val	Asn	Asn	Gln	Tyr	Thr	Val	Met	Phe	
	210					215					220					
Lys	Lys	Gly	Ala	Phe	Glu	Leu	Gly	Cys	Ala	Val	Cys	Pro	Ile	Ala	Ile	
225					230					235					240	
Lys	Tyr	Asn	Lys	Ile	Phe	Val	Asp	Ala	Phe	Trp	Asn	Ser	Lys	Lys	Gln	
				245				250						255		
Ser	Phe	Thr	Met	His	Leu	Val	Arg	Leu	Met	Thr	Ser	Trp	Ala	Val	Val	
			260					265					270			
Cys	Asp	Val	Trp	Tyr	Leu	Glu	Pro	Gln	Tyr	Leu	Arg	Glu	Gly	Glu	Thr	
		275					280					285				
Ala	Ile	Ala	Phe	Ala	Glu	Arg	Val	Arg	Asp	Met	Ile	Ala	Ala	Arg	Ala	
	290					295					300					
Gly	Leu	Lys	Lys	Val	Pro	Trp	Asp	Gly	Tyr	Leu	Lys	His	Asn	Arg	Pro	
305					310					315					320	
Ser	Pro	Lys	His	Thr	Glu	Glu	Lys	Gln	Arg	Ile	Phe	Ala	Glu	Ser	Val	
				325					330					335		

Leu Arg Arg Leu Glu Glu Lys  
340

<210> 33  
<211> 1466  
<212> DNA  
<213> Glycine max

<400> 33  
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ctttccttgt tagagttggg ttctgcaacc taccatgcaa ttcctcacct gaatccgttt 120  
tctattgcca cgttgggacg gaaaagtcta gtttaaccac acgtttgtgg ttgtagtgga 180  
agcgtaacga agatgaatgg cattgggaaa ctcaaatcgt cgagtcttga attggacctt 240  
cacattgaag attacctacc ttctggatcc agtgttcaac aagaacggca tggcaagctc 300  
cgactgtgtg atttgctaga catttctcct agtctatctg aggcagcacg tgccattgta 360  
gatgatacat tcacaagggtg cttcaagtca aatcctccag aaccttgga ctggaatggt 420  
tatttggttc ctttgtgggt ctgtggaggt gtggttcgat atttgatttt gttccctatt 480  
aggattctag tggtggcatt aggatggatt atatttcttt cagccttcat tccagtgcac 540  
tccctcctga aaggaaatga tgatttgagg aaaaagattg agagggtgtt ggtggagatg 600  
atgtgcagtt tctttgttgc atcatggact ggggttgta agtaccatgg gccaaagacct 660  
agtatccgac caaaacaggt ttttgtggcc aatcatactt ccatgattga tttcattatc 720  
ttagaacaga tgactgcatt tgctgttatt atgcagaagc atcctggatg ggttggatta 780  
ttgcagagca ccattttgga gagtgtgggg tgtatctggt tcaatcgtac agaggcaaag 840  
gatcgagaaa ttgtggcaag gaaattgagg gatcatgtcc tgggagctaa caataaccct 900  
cttctcatat ttcctgaagg aacttgtgta aataatcact actctgtcat gttcaagaag 960  
ggtgcatttg aacttggctg cacaatttgc ccagttgcaa tcaagtacaa taaaattttc 1020  
gtcgatgctt tttggaatag tcgaaagcaa tcattcacca ctcatctctt gcaattaatg 1080  
acatcttggg ctgtagtttg tgatgttttg tacttgagc caaaaattt gaagccagga 1140  
gagacacca ttgaatttgc agagagagtt agagacataa tctcacatcg tgctgggctt 1200  
aaaaagggtt cttgggatgg atatctgaag tattctcgcc ctagtcccaa gcacagagaa 1260  
ggaaagcaac aaatattcgc tgagtctgtg ttgcggcgct ttgaggaaaa ataatgtata 1320  
tctttttact ttttcagtaa tgattttctc caacccttgt ttgtactcca cttactacta 1380  
tgatatacat gtagatctta catgaaattg cctgaaaatt ttccatgacc aaaaaaaaaa 1440  
aaaaaaaaact cgagactagt tctctc 1466

<210> 34  
<211> 373  
<212> PRT  
<213> Glycine max

<400> 34  
Met Asn Gly Ile Gly Lys Leu Lys Ser Ser Ser Ser Glu Leu Asp Leu  
1 5 10 15  
His Ile Glu Asp Tyr Leu Pro Ser Gly Ser Ser Val Gln Gln Glu Arg  
20 25 30  
His Gly Lys Leu Arg Leu Cys Asp Leu Leu Asp Ile Ser Pro Ser Leu  
35 40 45  
Ser Glu Ala Ala Arg Ala Ile Val Asp Asp Thr Phe Thr Arg Cys Phe  
50 55 60  
Lys Ser Asn Pro Pro Glu Pro Trp Asn Trp Asn Val Tyr Leu Phe Pro  
65 70 75 80  
Leu Trp Cys Cys Gly Val Val Val Arg Tyr Leu Ile Leu Phe Pro Ile  
85 90 95

Arg	Ile	Leu	Val	Leu	Ala	Leu	Gly	Trp	Ile	Ile	Phe	Leu	Ser	Ala	Phe	
			100					105					110			
Ile	Pro	Val	His	Ser	Leu	Leu	Lys	Gly	Asn	Asp	Asp	Leu	Arg	Lys	Lys	
		115					120					125				
Ile	Glu	Arg	Cys	Leu	Val	Glu	Met	Met	Cys	Ser	Phe	Phe	Val	Ala	Ser	
	130					135					140					
Trp	Thr	Gly	Val	Val	Lys	Tyr	His	Gly	Pro	Arg	Pro	Ser	Ile	Arg	Pro	
145					150					155					160	
Lys	Gln	Val	Phe	Val	Ala	Asn	His	Thr	Ser	Met	Ile	Asp	Phe	Ile	Ile	
				165					170					175		
Leu	Glu	Gln	Met	Thr	Ala	Phe	Ala	Val	Ile	Met	Gln	Lys	His	Pro	Gly	
			180					185					190			
Trp	Val	Gly	Leu	Leu	Gln	Ser	Thr	Ile	Leu	Glu	Ser	Val	Gly	Cys	Ile	
		195					200					205				
Trp	Phe	Asn	Arg	Thr	Glu	Ala	Lys	Asp	Arg	Glu	Ile	Val	Ala	Arg	Lys	
	210					215					220					
Leu	Arg	Asp	His	Val	Leu	Gly	Ala	Asn	Asn	Asn	Pro	Leu	Leu	Ile	Phe	
225					230				235						240	
Pro	Glu	Gly	Thr	Cys	Val	Asn	Asn	His	Tyr	Ser	Val	Met	Phe	Lys	Lys	
				245					250					255		
Gly	Ala	Phe	Glu	Leu	Gly	Cys	Thr	Ile	Cys	Pro	Val	Ala	Ile	Lys	Tyr	
			260					265					270			
Asn	Lys	Ile	Phe	Val	Asp	Ala	Phe	Trp	Asn	Ser	Arg	Lys	Gln	Ser	Phe	
		275					280					285				
Thr	Thr	His	Leu	Leu	Gln	Leu	Met	Thr	Ser	Trp	Ala	Val	Val	Cys	Asp	
	290					295					300					
Val	Trp	Tyr	Leu	Glu	Pro	Gln	Asn	Leu	Lys	Pro	Gly	Glu	Thr	Pro	Ile	
305					310					315					320	
Glu	Phe	Ala	Glu	Arg	Val	Arg	Asp	Ile	Ile	Ser	His	Arg	Ala	Gly	Leu	
				325					330					335		
Lys	Lys	Val	Pro	Trp	Asp	Gly	Tyr	Leu	Lys	Tyr	Ser	Arg	Pro	Ser	Pro	
			340					345					350			
Lys	His	Arg	Glu	Gly	Lys	Gln	Gln	Ile	Phe	Ala	Glu	Ser	Val	Leu	Arg	
		355					360					365				
Arg	Phe	Glu	Glu	Lys												
			370													

<210> 35  
 <211> 1384  
 <212> DNA  
 <213> *Catalpa speciosa*



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<400> 35
gcacgaggta ggtttctgtc gaggatthttg ttgtttgttt tcgggttcta ttggattggt 60
gaaaccagta aggggaattga gggtgatggg caggggaata atgagtctgc atctaggaat 120
cggctctgaag aggtggaagg acctggggct attgtatcca atcatatatc ttatatagat 180
atcctgtatc acatgtcttc ctctttccca agtttcgtht ccaagagatc cgtcgctaaa 240
cttccccttg ttggtcttgt gagcaagtgt cttgggttgt tatatgtaca gcgtgagtta 300
aagtcgtcgg atttcaaggg ggtatcaggt gttgtcactg aaagaattca agaagctcat 360
caaaataagt ttgctccaaa gatgataatt ttcccagaag gcacaactac aaatggggac 420
ttcctccttc cattcaagac tgggtgcattt ttggcaaagg ctccagtact tcctgtcatt 480
ttaagatatt cgtaccagag atttagtccc gcgtgggact ctatttctgg ggctcgccat 540
gtgattcttc ttctctgtca gtttgtaaat tacattgaag tgacacattt gcctgtttat 600
catccgtccg aacaagaaaa ggaagatccc aagctthtct ctgaaaatgt taggcttctg 660
atggctcgtg agggtaattt gattctthtct gatattggat tggcggagaa acgagthtat 720
catgctgctc tcaatggtht actthtgcac agataatcca gcttcgctat attgattgta 780
taaatgtatt thttgacttc cataaaacta ataactaagc ccataaatta cgctggaaga 840
ggtcattgat cttcatcgtc tatacgattt ctaactatta tctggacatc ttagttactg 900
cttcagcttht ggtaaggatc ctctaaagct gtctctattt gatacattag gccgtctggc 960
ttaatacaga acgtggaagc cgatgttgta ttaacgacgt tggatgaacat ggagctattg 1020
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gagthctgtht gagattagcc ataaatcgca thtctctaac agthtgttct actgggtacg 1140
gtattagtht ccccttgat atagcacaaat gcaaatgctg tagttaacta cthtgttht 1200
atcttctgtt ttgtttgctt tattgcaacg ttaggagtht taaatatcct taaaatctag 1260
ttggattagc atagttaatt gtgaaatatg tagtggtgcc tgagaatggc cttggattgg 1320
aagthtctgct tcttctggga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1380
aaaa 1384

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<210> 36
<211> 251
<212> PRT
<213> Catalpa speciosa

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<400> 36
Ala Arg Gly Arg Phe Leu Ser Arg Ile Leu Leu Phe Val Phe Gly Phe
 1 5 10 15
Tyr Trp Ile Gly Glu Thr Ser Lys Gly Ile Glu Val Asp Gly Gln Gly
 20 25 30
Asn Asn Glu Ser Ala Ser Arg Asn Arg Ser Glu Glu Val Glu Gly Pro
 35 40 45
Gly Ala Ile Val Ser Asn His Ile Ser Tyr Ile Asp Ile Leu Tyr His
 50 55 60
Met Ser Ser Ser Phe Pro Ser Phe Val Ser Lys Arg Ser Val Ala Lys
 65 70 75 80
Leu Pro Leu Val Gly Leu Val Ser Lys Cys Leu Gly Cys Val Tyr Val
 85 90 95
Gln Arg Glu Leu Lys Ser Ser Asp Phe Lys Gly Val Ser Gly Val Val
 100 105 110
Thr Glu Arg Ile Gln Glu Ala His Gln Asn Lys Phe Ala Pro Lys Met
 115 120 125
Ile Ile Phe Pro Glu Gly Thr Thr Thr Asn Gly Asp Phe Leu Leu Pro
 130 135 140

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Phe Lys Thr Gly Ala Phe Leu Ala Lys Ala Pro Val Leu Pro Val Ile  
 145 150 155 160  
 Leu Arg Tyr Ser Tyr Gln Arg Phe Ser Pro Ala Trp Asp Ser Ile Ser  
 165 170 175  
 Gly Ala Arg His Val Ile Leu Leu Leu Cys Gln Phe Val Asn Tyr Ile  
 180 185 190  
 Glu Val Thr His Leu Pro Val Tyr His Pro Ser Glu Gln Glu Lys Glu  
 195 200 205  
 Asp Pro Lys Leu Phe Ala Glu Asn Val Arg Leu Leu Met Ala Arg Glu  
 210 215 220  
 Gly Asn Leu Ile Leu Ser Asp Ile Gly Leu Ala Glu Lys Arg Val Tyr  
 225 230 235 240  
 His Ala Ala Leu Asn Gly Leu Leu Cys Gln Arg  
 245 250

<210> 37  
 <211> 1042  
 <212> DNA  
 <213> Triticum aestivum

<400> 37  
 gcacgagcag gggttgagga gggaggccgt gctgcgtgct ggccgcgtgt tgctgcgggc 60  
 aatgctgttc gtgttcgggt tctactggat ccccggtgcc gatcgaagct tccccaatgc 120  
 cgaggatgta cctaaagatc actatgaaga actggaaaga ccagggggcga ttgtatctaa 180  
 tcatgtgtca tatgtggaca ttctttatca tatgtcagct tcttctccga gttttgttgc 240  
 taagaactca gtgtccaagt tgccggtgat tgggtctcata agcaaagtgc ttgggtgcat 300  
 ttttgttcaa cgagaatcca aatgttcaga ttctaaaggt gtctcaggtg ctgtaactga 360  
 aaggctccat gaggtttcac aagacgagaa ttcccctatg atcttactct ttcctgaggg 420  
 tactactacg aatggggatt accttctccc atttaagaca ggagccttctc ttgcaagggc 480  
 accattgcaa cctgtaattt tgagatatcc ttacaggaga tttagtccag cctgggactc 540  
 catggatggg gcacgtcatg tgtttttgct cctctgtcaa tttgcaaatt acatagaggt 600  
 ggttcgcttg cctgtatact atccttctga gcaagaaaag caggatccta gagtctatgc 660  
 caacaacgtc agaaaattgc ttgcgactga gggtaattta gttctgtcta atcttgggct 720  
 ggctgaaaag cgtgtgtatc atgcggcact taatggtaat agtcctcgtg ctctgcatca 780  
 gaaagatgat tgaaagccct tgcatactc tctgtacact atctgttgag gtgattgtaa 840  
 gaatgtatgc caacttttagc tgatcatgtg attcatgggt tctctgtttg aggagtatgt 900  
 tgattgatga aaacattata cctattttga gatgaattcc ctccttatac tacattgtat 960  
 agaaaccatt aaacattata gttcaataat aatgtctggc ataattgttt tgcttggtca 1020  
 aaaaaaaaaa aaaaaaaaaa aa 1042

<210> 38  
 <211> 261  
 <212> PRT  
 <213> Triticum aestivum

<400> 38  
 Gln Gly Leu Arg Arg Glu Ala Val Leu Arg Ala Gly Arg Val Leu Ser  
 1 5 10 15  
 Arg Ala Met Leu Phe Val Phe Gly Phe Tyr Trp Ile Pro Val Ser Asp  
 20 25 30  
 Arg Ser Phe Pro Asn Ala Glu Asp Val Pro Lys Asp His Tyr Glu Glu  
 35 40 45

Leu Glu Arg Pro Gly Ala Ile Val Ser Asn His Val Ser Tyr Val Asp  
 50 55 60  
 Ile Leu Tyr His Met Ser Ala Ser Ser Pro Ser Phe Val Ala Lys Asn  
 65 70 75 80  
 Ser Val Ser Lys Leu Pro Leu Ile Gly Leu Ile Ser Lys Cys Leu Gly  
 85 90 95  
 Cys Ile Phe Val Gln Arg Glu Ser Lys Cys Ser Asp Ser Lys Gly Val  
 100 105 110  
 Ser Gly Ala Val Thr Glu Arg Leu His Glu Val Ser Gln Asp Glu Asn  
 115 120 125  
 Ser Pro Met Ile Leu Leu Phe Pro Glu Gly Thr Thr Thr Asn Gly Asp  
 130 135 140  
 Tyr Leu Leu Pro Phe Lys Thr Gly Ala Phe Leu Ala Arg Ala Pro Leu  
 145 150 155 160  
 Gln Pro Val Ile Leu Arg Tyr Pro Tyr Arg Arg Phe Ser Pro Ala Trp  
 165 170 175  
 Asp Ser Met Asp Gly Ala Arg His Val Phe Leu Leu Leu Cys Gln Phe  
 180 185 190  
 Ala Asn Tyr Ile Glu Val Val Arg Leu Pro Val Tyr Tyr Pro Ser Glu  
 195 200 205  
 Gln Glu Lys Gln Asp Pro Arg Val Tyr Ala Asn Asn Val Arg Lys Leu  
 210 215 220  
 Leu Ala Thr Glu Gly Asn Leu Val Leu Ser Asn Leu Gly Leu Ala Glu  
 225 230 235 240  
 Lys Arg Val Tyr His Ala Ala Leu Asn Gly Asn Ser Pro Arg Ala Leu  
 245 250 255  
 His Gln Lys Asp Asp  
 260

<210> 39  
 <211> 1459  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> unsure  
 <222> (203)  
 <223> n = a, c, g, or t

<400> 39  
 gtttccaatc atatctcgta catagaaccc atattcttct tctatgaatt gttcccaacc 60  
 attgtttcgt cagagtctca tgatgcccta ccatttggtg gaacaattat tcgagcgatg 120  
 caggttatat atgttgacag attctcacca gcttctcgga aggctgctgt aaatgaaata 180  
 aagagaaagg cagcttgcaa tancctcccg cgggtcctgt tattccctga aggcaccaca 240  
 acaaatggga gattcctgat ttcgttccaa catgggtcgt tcatacctgg ctaccctgtt 300  
 caacctgttg ttgtccatta tccacatgtg cactttgatc aatcatgggg aaatatatcg 360

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ttattaaagc tcatgttcaa gatgttcaca cagtttcata atttcatgga ggtagagtag 420
cttcctgttg tctaccctcc tgagatcaag caagagaatg cccttcattt tgcagaggat 480
accagctatg ctatggcacg tgccctgaat gccttgccga cttattattc atggcgattc 540
tatgattatg gcacgagcag tagaagctgg aaaggtgaac tgctcaaatt atatggtaga 600
aatggcttgg gttaaagatg tttacggtat aagcacagca gaagtgatgg aactattgga 660
acatttcctg gctatgaatc cagataacga tggacgtgtg aaagctgaag atttctgggc 720
tcatttttgg ctggattgca gtcctctgtg caagaagata tttcactatt tcgatttaga 780
cattaagggg ttgattacgt tccgtcagtt cttgggttggg tgcgcgcacc tgaggaagca 840
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tgagatctcc agggcacagc tagctgatct cttgcggtta agcatgggtgc caccttctga 960
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ggacgacttc atggcgtgtc ttgggaggtt cccgttctct atcgcgttct ttgctgccct 1080
gatcaatggg gaagtgtaca tcgagatagt ctgaatgaat gcctgaggca aagcgatgcc 1140
gcgtaaaagg ctggagctgc cagtgccagg cgtaggcagg ggatccctcc gtttatgcaa 1200
tgtggatacc caccgggtgc tcctccactt tgagaccaa gcaactgtag tattgggtat 1260
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aattattatt ggccatttac cgaatctgtt gagatacgcg ctggactagt agattgtcga 1380
tggaactcag aacgcaaata gaaagcatct gtaatctgaa ctaactgaga aaacatttaa 1440
aaaaaaaaa aaaaaaaaaa 1459

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<210> 40
<211> 204
<212> PRT
<213> Zea mays

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<220>
<221> UNSURE
<222> (68)
<223> Xaa = any amino acid

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<400> 40
Val Ser Asn His Ile Ser Tyr Ile Glu Pro Ile Phe Phe Phe Tyr Glu
  1             5             10             15

Leu Phe Pro Thr Ile Val Ser Ser Glu Ser His Asp Ala Leu Pro Phe
          20             25             30

Val Gly Thr Ile Ile Arg Ala Met Gln Val Ile Tyr Val Asp Arg Phe
          35             40             45

Ser Pro Ala Ser Arg Lys Ala Ala Val Asn Glu Ile Lys Arg Lys Ala
          50             55             60

Ala Cys Asn Xaa Phe Pro Arg Val Leu Leu Phe Pro Glu Gly Thr Thr
          65             70             75             80

Thr Asn Gly Arg Phe Leu Ile Ser Phe Gln His Gly Ala Phe Ile Pro
          85             90             95

Gly Tyr Pro Val Gln Pro Val Val Val His Tyr Pro His Val His Phe
          100            105            110

Asp Gln Ser Trp Gly Asn Ile Ser Leu Leu Lys Leu Met Phe Lys Met
          115            120            125

Phe Thr Gln Phe His Asn Phe Met Glu Val Glu Tyr Leu Pro Val Val
          130            135            140

Tyr Pro Pro Glu Ile Lys Gln Glu Asn Ala Leu His Phe Ala Glu Asp
          145            150            155            160

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Thr Ser Tyr Ala Met Ala Arg Ala Leu Asn Ala Leu Pro Thr Tyr Tyr  
165 170 175

Ser Trp Arg Phe Tyr Asp Tyr Gly Thr Ser Ser Arg Ser Trp Lys Gly  
180 185 190

Glu Leu Leu Lys Leu Tyr Gly Arg Asn Gly Leu Gly  
195 200

<210> 41  
<211> 2115  
<212> DNA  
<213> Oryza sativa

<400> 41  
gcacgaggtt ctaaccgcgc tcctctcgcc tcgcctccgc caccatggc ttctcgaaac 60  
cctagccccc cctccctctc cagcccgctc ctctccgact ccatctcgcc cagcccacc 120  
accaacggcc acgcggggca ccataaccac gacgacgacg acgaggagtc gccaacgggtg 180  
tgccggcgcc atggcgagg agggggggac ccgttcgcgt tcctatcgga ggatcgggccg 240  
gcgtggtggt cgccgcgggg ggtgtccccg gccgacccgt tccgcaacgg gacgccgggg 300  
tggtgcgggg cgtacgagct cgtgagggcg ctctgtgtgc cgccggtggc ggcggcgagg 360  
ctggtgctgt tcgggctctc catcgcggtg gggtagccg ccacgtgggt ggcgctccgc 420  
gggtgggtcg acgtgcggga gcgggcggcg caggagggcg ccgggcccac gccggcggtg 480  
cgccgcccgc tcatgtggat cagcgggatc tccgcgcgct gcacccctct ctccctcgga 540  
taccattgga taaggaggaa aggaaaaccc gcgcctagag agcttgacc tatagttgct 600  
tcaaatacat tatcatacat agaaccata tacttcttct atgagctgtt cccgacaatc 660  
gtttcttcag attctcatga ttccatacca ttgtgtggaa caattatccg agcaatgcag 720  
gttatatatg ttgacagatt ctccgacgct tcaaggaagt ctgctgtaaa tgaaataaag 780  
gatgtgattt cagagaaagg cggcttgcaa tagcttccca cgtgtcttgt tattcccga 840  
aggcacgaca acaaatggaa gatttctgat ttctttccaa catggtgcat tcatacctgg 900  
ctaccctgtt caacctgtta ttgtgcgcta tccacatgtg cactttgatc aatcatgggg 960  
aaatatatca ttaggaaagc tcatgttcaa gatgtttacc cagtttcaca atttcatgga 1020  
ggtagagtac ctccctgttg ttaccaccac tgagatcaag caagagaatg cccttcattt 1080  
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ggcactcttg gaagactttt tgtgtatgag cccagacaag gacggacgtg tgaatgcgca 1320  
agatttttgg gctcattttg gccttaattg caccctctt tgcaagaaga tatttcagta 1380  
cttcgatttt gaagccaagg aatccatcac attccgtcag ttcttgattg gatgtgcgca 1440  
cctcaggaag cagccatcgt ttcaggacgc ctgcgaaacc gcgtttgaga ggtgtaggaa 1500  
tcccctaaca tctcacatcg gcaggagaca gctcgccgat gtcctgcggt caagcatgct 1560  
tgagctgatg accgataatg ggatgatgaa gctgttcaag acgttggacg tcgacgatga 1620  
cgacggaatc agcaaggatg acctgatggc atcccttagg aagctcccct tcatgatcgc 1680  
gctcttcgcg ggccggatca acggggaagt ctacatcgag atagtttgat cgactggatt 1740  
gatcgagggg gagagcaaaa atggtggatg ggagtttgta acgcgggtggg agacgacaga 1800  
cctccgtctg tttttagagg gatggtttcc aaccgcttca ccgtccatgt agctttctca 1860  
ggcgtggttg actaaagtgg ctaaccggta tagtgcgcaa ttttgtttca tatcgtaaaa 1920  
atatatatat atatccatag aaaagctgtc gcgtgatggc acgctggatt gtgcaatgtg 1980  
gatatgatac tgtacaacat tgggtccaact gggcgtgcac atagaaactc tttttttggt 2040  
ttggtttggt ttggctaact ggatggatga ttacaaactc ctttttggct aaaaaaaaaa 2100  
aaaaaaaaaa aaaaaa 2115

<210> 42  
<211> 255  
<212> PRT  
<213> Oryza sativa

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<400> 42
Met Ala Ser Arg Asn Pro Ser Pro Ala Ser Leu Ser Thr Pro Leu Leu
 1          5          10          15

Ser Asp Ser Ile Ser Pro Thr Pro Thr Thr Asn Gly His Ala Gly His
      20          25          30

His Asn His Asp Asp Asp Asp Glu Glu Ser Pro Thr Val Cys Gly Gly
      35          40          45

Asp Gly Gly Gly Gly Gly Asp Pro Phe Ala Phe Leu Ser Glu Asp Arg
      50          55          60

Pro Ala Trp Trp Ser Pro Arg Gly Val Ser Pro Ala Asp Pro Phe Arg
      65          70          75          80

Asn Gly Thr Pro Gly Trp Cys Gly Ala Tyr Glu Leu Val Arg Ala Leu
      85          90          95

Val Cys Ala Pro Val Ala Ala Ala Arg Leu Val Leu Phe Gly Leu Ser
      100          105          110

Ile Ala Val Gly Tyr Ala Ala Thr Trp Val Ala Leu Arg Gly Trp Val
      115          120          125

Asp Val Arg Glu Arg Ala Ala Gln Glu Gly Ala Gly Pro Met Pro Ala
      130          135          140

Trp Arg Arg Arg Leu Met Trp Ile Thr Arg Ile Ser Ala Arg Cys Ile
      145          150          155          160

Leu Phe Ser Phe Gly Tyr His Trp Ile Arg Arg Lys Gly Lys Pro Ala
      165          170          175

Pro Arg Glu Leu Ala Pro Ile Val Val Ser Asn His Val Ser Tyr Ile
      180          185          190

Glu Pro Ile Tyr Phe Phe Tyr Glu Leu Phe Pro Thr Ile Val Ser Ser
      195          200          205

Asp Ser His Asp Ser Ile Pro Phe Val Gly Thr Ile Ile Arg Ala Met
      210          215          220

Gln Val Ile Tyr Val Asp Arg Phe Ser Pro Ala Ser Arg Lys Ser Ala
      225          230          235          240

Val Asn Glu Ile Lys Asp Val Ile Ser Glu Lys Gly Gly Leu Gln
      245          250          255

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<210> 43
<211> 2041
<212> DNA
<213> Glycine max

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<400> 43
gcacgaggcg acgacgacga cttctccgtg ccgccaccgt ccaccctgga cccgttcgcg 60
aaccgcacgc cggcgatcga ggggctctac gagtgggcca agacggcgct gtgcctgccg 120
ctggcgggcg tgcggctcgc gctgttcggg ctctgcctcg cgggtgggta cgtggcgacg 180
aaggtggcgc tggcagggtg gaaggacaag gagaatccca tgcccaagtg gaggtgtagg 240
gttatgtgga tcacgcgctt gtgcgccaga tgtattctct tctcctttgg ctatcagtgg 300

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ataaaacgga aaggaaaacc tgcaccaagg gaaattgctc caataattgt atctaaccat 360
gtttcttata ttgagcctat cttctatttc tatgaattat ttcctaccat tgtggcagct 420
gagtctcatg actccatacc ttttggtggc accattatta gagcaatgca ggtcatatat 480
gttaacagat tcttaccatc atcaaggaag caggctgtta gggaaataaa gaaatctgct 540
ttcaaggaac tgaataacag agaagggcct cttgtgataa atttcctcga gtactattat 600
ttcccagagg aacaacaact aatggcagga accttatctc cttccaactt ggtgcattta 660
tccctgggata cccaatccag cctgtaatta tacgctatcc tcatgtacac tttgaccaat 720
cctggggtaa tgtttctttg ggaaagctta tgttcagaat gttcactcaa tttcacaact 780
tttttgaggt agaatatctt cctgtcattt atcccctgga tgataaggaa actgctgtac 840
attttcggga gaggactagc cgtgctatcg caactgcact aaatgctgtc cagacaggac 900
attcttatgg agacataatg cttcatatga aagcacaaga agcaaaacag gagaaccctt 960
caagttttat ggttgaaatg accaagggtg aatcattatt tcatatcagc agcacggaag 1020
ctgtggactt tctggataaa ttcttggcca tgaatcctga tcccagtggt cgtgttcaat 1080
atcatgactt cttgagggtt ttaagactta aggcttgccc actatctgca aagatatattt 1140
cattcattga tgtggagaag agtgggacaa ttacgttcag acagttcttg tatggatctg 1200
cccatgttat gtcccaacct gggttcgatc aaacctttga agaagccttt gctggctgtg 1260
gcggtgcagt aaagacctat gttgttgaac aagagttacg agatttcac ccaacctgct 1320
tcctcaattg gagtgaggat gaggtccatg agttttttat gttatttgac aatgataatg 1380
atggaagaat tgacaagaat gactttcttt catgccttag aagaaatcct cttctcatag 1440
cattttttac acctcagcca cagcaaaaag aatttgaagg taatggagtg atagaaatag 1500
tgtgatggat ggatttcaca ttcaggctct ttgtggacta caaagaaaag aaatgggtag 1560
ggattcctgg ggaatacata cagtatagga tgcagtggcc tcattttttt ttttttttcc 1620
ttttctcttt taattttttt accttgctct gattaattac tcgtaaagca taactatttg 1680
gtgaagatct gtgccatcca tcctgcttca tttgatgttt tttgttagct aggtcagttt 1740
tgcacagcta gatgtcagtt acctggatgt tgtgatcaca ccatccaac atttgagttt 1800
tggttcaggg accatgctga catttagggt ccatgtggtt catgtaaagt ttgaaccaac 1860
gtgtcaattt gtaacaaaca ttataactgt attttttttc aaagatgtga acatgaagaa 1920
agtaatgtaa tttatttgga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaactcgag 1980
ggggggcccg gttgttttcg aggtcgacgt gctcgataag attgtatcca caccgagcgc 2040
g 2041

```

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<210> 44
<211> 228
<212> PRT
<213> Glycine max

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<400> 44
Ala Arg Gly Asp Asp Asp Asp Phe Ser Val Pro Pro Pro Ser Thr Leu
 1 5 10 15
Asp Pro Phe Arg Asn Arg Thr Pro Ala Ile Glu Gly Leu Tyr Glu Trp
 20 25 30
Ala Lys Thr Ala Leu Cys Leu Pro Leu Ala Ala Leu Arg Leu Ala Leu
 35 40 45
Phe Gly Leu Cys Leu Ala Val Gly Tyr Val Ala Thr Lys Val Ala Leu
 50 55 60
Ala Gly Trp Lys Asp Lys Glu Asn Pro Met Pro Lys Trp Arg Cys Arg
 65 70 75 80
Val Met Trp Ile Thr Arg Leu Cys Ala Arg Cys Ile Leu Phe Ser Phe
 85 90 95
Gly Tyr Gln Trp Ile Lys Arg Lys Gly Lys Pro Ala Pro Arg Glu Ile
 100 105 110
Ala Pro Ile Ile Val Ser Asn His Val Ser Tyr Ile Glu Pro Ile Phe
 115 120 125

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Tyr Phe Tyr Glu Leu Phe Pro Thr Ile Val Ala Ala Glu Ser His Asp  
 130 135 140  
 Ser Ile Pro Phe Val Gly Thr Ile Ile Arg Ala Met Gln Val Ile Tyr  
 145 150 155 160  
 Val Asn Arg Phe Leu Pro Ser Ser Arg Lys Gln Ala Val Arg Glu Ile  
 165 170 175  
 Lys Lys Ser Ala Phe Lys Glu Leu Asn Asn Arg Glu Gly Pro Leu Val  
 180 185 190  
 Ile Asn Phe Leu Glu Tyr Tyr Tyr Phe Pro Arg Glu Gln Gln Leu Met  
 195 200 205  
 Ala Gly Thr Leu Ser Pro Ser Asn Leu Val His Leu Ser Leu Asp Thr  
 210 215 220

Gln Ser Ser Leu  
225

<210> 45  
 <211> 1502  
 <212> DNA  
 <213> Zea mays

<400> 45  
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 gagcgtgggc ggcagtgaga tgagcagcga agacatggcc gccgccagtc cgctcctctc 180  
 gtcgtcctcc ccctccctt cccctccgc agccccgggtg ctggagagca tagaggaact 240  
 ggaccggaag tacgcaccgt acgcgcggcg ggacgcgtac ggaccgatgg ggctcggccc 300  
 cgtgagcgca gcggaggctg cgcggctggc gtttgccgcg gtcgtgctgg tcccgcctccg 360  
 tgtcgtggca ggtgttctcg tactcgtggt ctactacctc gtgtgccgcg tgtgcacgct 420  
 gcgggtggag gaggaccggg agggcgccga aggggatggg tacgcgcggg tggacgggtg 480  
 gaggcgggcg ggggctgtgc ggtgcggccg cgcactcgct cgcgccatgt tgtttgtctt 540  
 cgggttctat tggatccgag agtacgacag ccgccttccc aatgctgagg atggccatgt 600  
 ggaccagtct aaagaaatcg aaaggcctgg ggcaattgtg tctaatacatg tatcttatgt 660  
 ggatattctt tatcacatgt cagcctcttt tcctagtttt gttgctaaga gatcagtggc 720  
 tagattgcct ctagttggtc tcataagcaa atgtcttgga tgcatttttg ttcagcggga 780  
 gtcgaaaaca ccagatttca aagggtgtttc aggtgctgta tctgaaagaa tccatcgtgc 840  
 tcatcaacag aaaaatgcac caatgatgct actcttccct gagggcacia ctacaaatgg 900  
 ggattatctc ctccattca aaacagggtgc ttttcttgca aaggcaccag ttcaaccagt 960  
 cattttgaga tatccttaca aaagatttaa tgcagcatgg gattccatgt caggggcacg 1020  
 tcatgtattt ctgctgctct gtcaatttgt aaattaccta gaggtgggtc gcttaccagt 1080  
 ttactatcct tctgagcaag aaaaggatga tcctaagctc tatgcaaaca atgtacggaa 1140  
 actgatggca gtggagggaa acttgattct ttcagacctt gggctggcgg agaagcgagt 1200  
 gtaccatgcc gcactgaatg gtaatagtct agctcgtgct ttacatcaga aagatgattg 1260  
 aaatgccatg ctatcgtgct tccataatac tggcttgctt gtaactgtgt gcttgcttgt 1320  
 gcatcgtcat ggttgagagg aatgtcgtga atatactatc cggcataaat ctgtaaagta 1380  
 atttaccacac tgtcatagtt cagtaattat gttgggtata ctctacatg gttgggcatc 1440  
 cgcacatttg atcctgtggt caatccatgt gagccttttt tactaaaaaa aaaaaaaaaa 1500  
 aa 1502

<210> 46  
 <211> 395  
 <212> PRT  
 <213> Zea mays



<400> 46

Met	Ala	Pro	Asn	Glu	Ala	Ala	Ser	Ile	Thr	Thr	Pro	Ser	Glu	Pro	Glu			
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Ser	Val	Gly	Gly	Ser	Glu	Met	Ser	Ser	Glu	Asp	Met	Ala	Ala	Ala	Ser			
			20					25					30					
Pro	Leu	Leu	Ser	Ser	Ser	Ser	Pro	Ser	Pro	Ser	Pro	Ser	Ala	Ala	Pro			
		35					40					45						
Val	Leu	Glu	Ser	Ile	Glu	Glu	Leu	Asp	Arg	Lys	Tyr	Ala	Pro	Tyr	Ala			
	50					55					60							
Arg	Arg	Asp	Ala	Tyr	Gly	Pro	Met	Gly	Leu	Gly	Pro	Val	Ser	Ala	Ala			
65					70					75					80			
Glu	Ala	Ala	Arg	Leu	Ala	Phe	Ala	Ala	Val	Val	Leu	Val	Pro	Leu	Arg			
				85					90					95				
Val	Val	Ala	Gly	Val	Leu	Val	Leu	Val	Val	Tyr	Tyr	Leu	Val	Cys	Arg			
			100					105					110					
Val	Cys	Thr	Leu	Arg	Val	Glu	Glu	Asp	Arg	Glu	Gly	Gly	Glu	Gly	Asp			
		115					120					125						
Gly	Tyr	Ala	Arg	Leu	Asp	Gly	Trp	Arg	Arg	Ala	Gly	Ala	Val	Arg	Cys			
	130					135					140							
Gly	Arg	Ala	Leu	Ala	Arg	Ala	Met	Leu	Phe	Val	Phe	Gly	Phe	Tyr	Trp			
145					150					155					160			
Ile	Arg	Glu	Tyr	Asp	Ser	Arg	Leu	Pro	Asn	Ala	Glu	Asp	Gly	His	Val			
				165					170					175				
Asp	Gln	Ser	Lys	Glu	Ile	Glu	Arg	Pro	Gly	Ala	Ile	Val	Ser	Asn	His			
			180					185					190					
Val	Ser	Tyr	Val	Asp	Ile	Leu	Tyr	His	Met	Ser	Ala	Ser	Phe	Pro	Ser			
		195					200					205						
Phe	Val	Ala	Lys	Arg	Ser	Val	Ala	Arg	Leu	Pro	Leu	Val	Gly	Leu	Ile			
	210					215					220							
Ser	Lys	Cys	Leu	Gly	Cys	Ile	Phe	Val	Gln	Arg	Glu	Ser	Lys	Thr	Pro			
225					230					235					240			
Asp	Phe	Lys	Gly	Val	Ser	Gly	Ala	Val	Ser	Glu	Arg	Ile	His	Arg	Ala			
				245					250					255				
His	Gln	Gln	Lys	Asn	Ala	Pro	Met	Met	Leu	Leu	Phe	Pro	Glu	Gly	Thr			
			260					265					270					
Thr	Thr	Asn	Gly	Asp	Tyr	Leu	Leu	Pro	Phe	Lys	Thr	Gly	Ala	Phe	Leu			
		275					280					285						
Ala	Lys	Ala	Pro	Val	Gln	Pro	Val	Ile	Leu	Arg	Tyr	Pro	Tyr	Lys	Arg			
	290					295					300							
Phe	Asn	Ala	Ala	Trp	Asp	Ser	Met	Ser	Gly	Ala	Arg	His	Val	Phe	Leu			
305					310					315					320			

Leu Leu Cys Gln Phe Val Asn Tyr Leu Glu Val Val Arg Leu Pro Val  
325 330 335

Tyr Tyr Pro Ser Glu Gln Glu Lys Asp Asp Pro Lys Leu Tyr Ala Asn  
340 345 350

Asn Val Arg Lys Leu Met Ala Val Glu Gly Asn Leu Ile Leu Ser Asp  
355 360 365

Leu Gly Leu Ala Glu Lys Arg Val Tyr His Ala Ala Leu Asn Gly Asn  
370 375 380

Ser Leu Ala Arg Ala Leu His Gln Lys Asp Asp  
385 390 395

<210> 47  
<211> 1555  
<212> DNA  
<213> Oryza sativa

<400> 47  
gcacgaggtt taaaccacgt ctctctcgcca tctcctcatg cctacccact gctaggggttt 60  
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ccctccgacc ccgacgacct cggcgggcggc ggcgaggagg aggaggagag gctcgcctcg 180  
aagccgctgc tctcgtcccc gtccacctat ccttccgcgg ggacggagga gggcgctcgag 240  
gagctggagc tcgaccggag gtacgcgccg tacgcgaggc gggacgcgta cggggcgatg 300  
ggccggggcc ccctggggcgc ggcggggggcg gggcggtctg cgggtgggcgc cgccgtgctc 360  
ttcccgtctc ggctcgccgc gggcggtgctc gtgctcgtcg cctactacct cgtgtgccgc 420  
gtgtgcacgc tgcgtgtgga ggaggaggag cgcgagggtg gcggtggcgc cgcggtgga 480  
gaagtggagg gggacgggta cgcgcggctc gaggggtgga ggcgtgaggc cgtcgtgcgc 540  
tgcggccgcg cgctcgcgcg cgccatgctg ttcgtcttcg gcttctactg gatccgcgag 600  
tacgactgcc gcttccctga tgctgaggat gagcatcagg aacagtccaa agaattggga 660  
agaccagggg cagtagtata taatcatgta tcttatgtgg atattcttta ccacatgtca 720  
tcttccttcc caagctttgt tgccaagaga tcagtggcca gattgccccat ggttgggtctc 780  
ataagcaaat gtcttggatg catttttgtt cagcgggaat ctaaaacctc agatttcaaa 840  
ggcgtttcag gtgctgtgac tgagagaatc caacgggctc atcaacagaa gaattctcca 900  
atgatgctac ttttccctga aggcacaact acaaatggtg attatctcct ccctttcaag 960  
acaggagcat ttcttgcaaa agcaccagtg aagccagtca ttttaagata tccttacaag 1020  
agatttagtc cagcatggga ttcgatgtct ggggctcggc atgtatttct gctcctttgt 1080  
caatttgtaa ataacctga ggtgatccat ttgcctgtgt attacccatc tgagcaagag 1140  
aaggaagatc ctaagctgta cgcaaataat gtacggaaat tgatggcagt ggaggggaac 1200  
ttgattcttt ctgatcttgg gctagcagag aagcgtgtgt accatgcggc attgaatgg 1260  
aataatagtc tacctcgtgc tttacatcag aaagatgatt gaaatgcctt gccatcgcgc 1320  
ttctgtatac tgatgctgag tgacttgctt gtaatatgag tacaagtcc tggtgttgca 1380  
tgattcctca tggtgagagg agctatgtta atatcctccc agtaaactgt aaaattattt 1440  
gtccatagtg tggttcagta atcatgtcag ttatacatga ttacattcac atgtctggga 1500  
cacacttcac catgcaatcc atcgatgtga gctttataaa aaaaaaaaaa aaaaa 1555

<210> 48  
<211> 404  
<212> PRT  
<213> Oryza sativa

<400> 48  
Met Ala Leu Pro Leu His Asp Ala Thr Thr Ser Pro Ser Asp Pro Asp  
1 5 10 15

Asp Leu Gly Gly Gly Gly Glu Glu Glu Glu Glu Arg Leu Ala Ser Lys  
20 25 30

Pro	Leu	Leu	Ser	Ser	Pro	Ser	Thr	Tyr	Pro	Ser	Ala	Gly	Thr	Glu	Glu			
		35					40					45						
Gly	Val	Glu	Glu	Leu	Glu	Leu	Asp	Arg	Arg	Tyr	Ala	Pro	Tyr	Ala	Arg			
	50					55					60							
Arg	Asp	Ala	Tyr	Gly	Ala	Met	Gly	Arg	Gly	Pro	Leu	Gly	Ala	Ala	Gly			
65					70					75					80			
Ala	Gly	Arg	Leu	Ala	Val	Gly	Ala	Ala	Val	Leu	Phe	Pro	Leu	Arg	Leu			
				85					90					95				
Ala	Ala	Gly	Val	Leu	Val	Leu	Val	Ala	Tyr	Tyr	Leu	Val	Cys	Arg	Val			
			100					105					110					
Cys	Thr	Leu	Arg	Val	Glu	Glu	Glu	Glu	Arg	Glu	Gly	Gly	Gly	Gly	Gly			
	115					120						125						
Ala	Ala	Gly	Glu	Val	Glu	Gly	Asp	Gly	Tyr	Ala	Arg	Leu	Glu	Gly	Trp			
	130					135					140							
Arg	Arg	Glu	Gly	Val	Val	Arg	Cys	Gly	Arg	Ala	Leu	Ala	Arg	Ala	Met			
145					150					155					160			
Leu	Phe	Val	Phe	Gly	Phe	Tyr	Trp	Ile	Arg	Glu	Tyr	Asp	Cys	Arg	Phe			
			165						170					175				
Pro	Asp	Ala	Glu	Asp	Glu	His	Gln	Glu	Gln	Ser	Lys	Glu	Leu	Gly	Arg			
			180					185						190				
Pro	Gly	Ala	Val	Val	Ser	Asn	His	Val	Ser	Tyr	Val	Asp	Ile	Leu	Tyr			
	195					200						205						
His	Met	Ser	Ser	Ser	Phe	Pro	Ser	Phe	Val	Ala	Lys	Arg	Ser	Val	Ala			
	210					215					220							
Arg	Leu	Pro	Met	Val	Gly	Leu	Ile	Ser	Lys	Cys	Leu	Gly	Cys	Ile	Phe			
225					230					235					240			
Val	Gln	Arg	Glu	Ser	Lys	Thr	Ser	Asp	Phe	Lys	Gly	Val	Ser	Gly	Ala			
				245					250					255				
Val	Thr	Glu	Arg	Ile	Gln	Arg	Ala	His	Gln	Gln	Lys	Asn	Ser	Pro	Met			
			260					265					270					
Met	Leu	Leu	Phe	Pro	Glu	Gly	Thr	Thr	Thr	Asn	Gly	Asp	Tyr	Leu	Leu			
	275					280						285						
Pro	Phe	Lys	Thr	Gly	Ala	Phe	Leu	Ala	Lys	Ala	Pro	Val	Lys	Pro	Val			
	290				295						300							
Ile	Leu	Arg	Tyr	Pro	Tyr	Lys	Arg	Phe	Ser	Pro	Ala	Trp	Asp	Ser	Met			
305					310					315					320			
Ser	Gly	Ala	Arg	His	Val	Phe	Leu	Leu	Leu	Cys	Gln	Phe	Val	Asn	Asn			
				325					330					335				
Leu	Glu	Val	Ile	His	Leu	Pro	Val	Tyr	Tyr	Pro	Ser	Glu	Gln	Glu	Lys			
			340					345					350					

Glu Asp Pro Lys Leu Tyr Ala Asn Asn Val Arg Lys Leu Met Ala Val  
 355 360 365

Glu Gly Asn Leu Ile Leu Ser Asp Leu Gly Leu Ala Glu Lys Arg Val  
 370 375 380

Tyr His Ala Ala Leu Asn Gly Asn Asn Ser Leu Pro Arg Ala Leu His  
 385 390 395 400

Gln Lys Asp Asp

<210> 49  
 <211> 1072  
 <212> DNA  
 <213> Glycine max

<400> 49  
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 actctgcctc tcaggaagac cggagtcagc ctgaagagtt ggggagacct agcgtataaa 180  
 tatctaatac tgtgtcatac ttggatattt tgtatcacat gtcgtcctca ttcccaagtt 240  
 ttgttgctaa gagatcagtg gctaaacttc cgctcattgg tctcatcagc aagtgccttg 300  
 gttgtgtgta tggttcagcgg gaatcaaagt catcggactt caagggtgtt tcagctgttg 360  
 tcaactgacag aattcaagaa gctcatcaga atgagtcctgc tccattaatg atgttatttc 420  
 cagaaggaac aaccacaaat ggagagttcc tccttcatt caagactggg ggtttttttg 480  
 caaaggcacc agtacttcct gtgattttta gatatcatta ccagagattt agccccgcct 540  
 gggattccat atctgggggtg cgccatgtaa tatttctcct gtgtcagttt gtgaattata 600  
 tggaggtgat ccgagtacct gtttaccatc cctcacagca ggagatgaat gatcccaaac 660  
 tatatgctaa taatgttaga aggttgatgg ctactgaggg taatttgata ctttctgata 720  
 ttgggttagc tgaaaaacga atatatcacg ctgctctcaa tggtaataat agcatgccta 780  
 gtgttttgca tcagaaagac gaatgataat ttcatggccc ccgtctcaaa tgaaatgtag 840  
 ttccagtcga gtttttagttt caaacttagt atctgtttat gaatggacag cttgtgtgaa 900  
 gggatatagc aaatagtata cattcaccta aacatctgaa tggactttgt gtaattttct 960  
 tgtaaataac gtgaccaata atgttttaat tgctgggtgaa ctcaatttga ggcacacaat 1020  
 tcaagatcta taagttaaac tggtcttcgt tcaaaaaaaaa aaaaaaaaaa aa 1072

<210> 50  
 <211> 267  
 <212> PRT  
 <213> Glycine max

<400> 50  
 Thr Arg Glu Asp Tyr Ala His Met Ser Gly Leu Arg Arg Thr Val Ile  
 1 5 10 15  
 Val Ser Cys Gly Arg Ala Leu Ser Arg Val Met Leu Phe Ile Phe Gly  
 20 25 30  
 Phe Tyr Trp Ile Pro Glu Ser Asn Ser Ala Ser Gln Glu Asp Arg Ser  
 35 40 45  
 Gln Pro Glu Glu Leu Gly Arg Pro Ser Val Ile Ile Ser Asn His Val  
 50 55 60  
 Ser Tyr Leu Asp Ile Leu Tyr His Met Ser Ser Ser Phe Pro Ser Phe  
 65 70 75 80

Val	Ala	Lys	Arg	Ser	Val	Ala	Lys	Leu	Pro	Leu	Ile	Gly	Leu	Ile	Ser		
				85					90					95			
Lys	Cys	Leu	Gly	Cys	Val	Tyr	Val	Gln	Arg	Glu	Ser	Lys	Ser	Ser	Asp		
			100					105					110				
Phe	Lys	Gly	Val	Ser	Ala	Val	Val	Thr	Asp	Arg	Ile	Gln	Glu	Ala	His		
		115					120					125					
Gln	Asn	Glu	Ser	Ala	Pro	Leu	Met	Met	Leu	Phe	Pro	Glu	Gly	Thr	Thr		
	130					135					140						
Thr	Asn	Gly	Glu	Phe	Leu	Leu	Pro	Phe	Lys	Thr	Gly	Gly	Phe	Leu	Ala		
145					150					155					160		
Lys	Ala	Pro	Val	Leu	Pro	Val	Ile	Leu	Arg	Tyr	His	Tyr	Gln	Arg	Phe		
				165					170					175			
Ser	Pro	Ala	Trp	Asp	Ser	Ile	Ser	Gly	Val	Arg	His	Val	Ile	Phe	Leu		
			180					185					190				
Leu	Cys	Gln	Phe	Val	Asn	Tyr	Met	Glu	Val	Ile	Arg	Val	Pro	Val	Tyr		
		195					200					205					
His	Pro	Ser	Gln	Gln	Glu	Met	Asn	Asp	Pro	Lys	Leu	Tyr	Ala	Asn	Asn		
	210					215					220						
Val	Arg	Arg	Leu	Met	Ala	Thr	Glu	Gly	Asn	Leu	Ile	Leu	Ser	Asp	Ile		
225					230					235					240		
Gly	Leu	Ala	Glu	Lys	Arg	Ile	Tyr	His	Ala	Ala	Leu	Asn	Gly	Asn	Asn		
				245					250					255			
Ser	Met	Pro	Ser	Val	Leu	His	Gln	Lys	Asp	Glu							
			260					265									

<210> 51  
 <211> 838  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> unsure  
 <222> (205)  
 <223> n = a, c, g, or t

<220>  
 <221> unsure  
 <222> (779)  
 <223> n = a, c, g, or t

<220>  
 <221> unsure  
 <222> (814)  
 <223> n = a, c, g, or t

<400> 51  
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 tgttaacaga ttcttaccat catcaaggaa gcaggctgtt agggaaataa agagaagggc 120  
 ctcttgcaat agatttcctc gagtactatt atttcccagag ggaacaacaa caaatggcag 180

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gaaccttatac tccttccaac ttggngcatt tatccctgga tacccaatcc agcctgtaat 240
tgtacgctat cctcatgtgc actttgacca atcctgggggt catgtttctt tgggaaagct 300
tatgttcaga atgttcactc aatttcacaa cttttttgag gtagaatatc ttcctgtcat 360
ttatcccctg gatgataagg aaactgctgt acattttcgg gagaggacta gccgtgctat 420
cgcaactgca ctaaagtctg tccagacagg acattcttat ggagacataa tgcttcatat 480
gaaagcacaa gaagcaaaac aggagaaccc ctcaagtttt atgggttgaaa tgaccaaggt 540
ggaatcagtg agtccctaaa agcaaatgac cttaccattt cttttttttt tctgccattt 600
tcaagtccct tgtaaattat cttttttctt aactttttta gtaggatatt taggttaaac 660
cttttgaagt acatgcaa at gccacagtaa ccctttgctt atgccaatgg atgacagaca 720
taagtgaccc aggggtggctg cataatgttg gggccttcta atctatggga aatatgtant 780
gaaaggggag aatatttaaa ttgtgatttg tggnaataag gggataatat gacataag 838

```

```

<210> 52
<211> 185
<212> PRT
<213> Glycine max

```

```

<400> 52
Arg Glu Leu Val Ser Ala Ile Phe His Phe Phe Pro Leu Leu Cys Phe
 1          5          10          15

Gln Val Ile Tyr Val Asn Arg Phe Leu Pro Ser Ser Arg Lys Gln Ala
 20          25          30

Val Arg Glu Ile Lys Arg Arg Ala Ser Cys Asn Arg Phe Pro Arg Val
 35          40          45

Leu Leu Phe Pro Glu Gly Thr Thr Thr Asn Gly Arg Asn Leu Ile Ser
 50          55          60

Phe Gln Leu Gly Ala Phe Ile Pro Gly Tyr Pro Ile Gln Pro Val Ile
 65          70          75          80

Val Arg Tyr Pro His Val His Phe Asp Gln Ser Trp Gly His Val Ser
 85          90          95

Leu Gly Lys Leu Met Phe Arg Met Phe Thr Gln Phe His Asn Phe Phe
100          105          110

Glu Val Glu Tyr Leu Pro Val Ile Tyr Pro Leu Asp Asp Lys Glu Thr
115          120          125

Ala Val His Phe Arg Glu Arg Thr Ser Arg Ala Ile Ala Thr Ala Leu
130          135          140

Asn Ala Val Gln Thr Gly His Ser Tyr Gly Asp Ile Met Leu His Met
145          150          155          160

Lys Ala Gln Glu Ala Lys Gln Glu Asn Pro Ser Ser Phe Met Val Glu
165          170          175

Met Thr Lys Val Glu Ser Val Ser Pro
180          185

```

```

<210> 53
<211> 1632
<212> DNA
<213> Oryza sativa

```

```

<400> 53
cttctcgtcg ccggtggatt cgccgccgcc tccgccgccg ccgccggagg aggaggacga 60
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catctcggcc ccgcgagatt ggaagtgagg gcagggcagg gcggcagggg ccatggcggt 180
cccactcgtg ctcgtcgtgc tcccgctcgg cctcctcttc ctctctccg gcctcatcat 240
caacgccatc caggccgtcc tgtttctctc gataaggccg ttctcgaaga gcttgtaccg 300
gcggtatcaac aggttcttgg ccgagctgct gtggcttcag ctgggtctggc ttgtggattg 360
gtgggcagga gttaagatac aactgcatgc tgatgacgaa acttacaagg caatggggaa 420
tgagcatgca cttgtcatat caaataatcg gagcgatata gattggctta ttgggtggat 480
tttggcacag cgctcaggat gccttggaag tacacttgct gttatgaaga aatcatcgaa 540
attccttcca gttattggct ggtccatgtg gtttgcagaa tacctctttt tggaaaggag 600
ctgggcaaag gatgaaaaga cattgaaatg gggcctccaa aggttgaagg acttccccag 660
accatttttg ctagcccttt ttgttgaggg cactcgcttt actccagcaa agcttctagc 720
agctcaggag tatgctgttt cacagggttt gccagcacc agaaatgtat tgattccacg 780
tacaaggga tttgtatcag ctgtaactat tatgcgggat tttgttccag ctatttatga 840
tacaacagta attattccaa aagattcacc tcaaccaaca atgctgcgga ttttgaaagg 900
gcaatcttca gtggtacatg ttcgcatgaa acgtcatgca atgagtgaga tgccaaagtc 960
agaagacgat gtttcaaaat ggtgcaaaga catctttgta gcaaaggatg cattactgga 1020
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atcattgctg gtgactttgt tttggtcatg tctcctttta tatggcgccg tcaagctctt 1140
cctatggact caactcctgt cgacatggaa aggagtccggg ttacggggc ttgggctcgc 1200
actggtgacg gcggtcatgc atgtcttcat catgttctcg cagtcagagc gatcgagctc 1260
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gcttatcaat gggagctacc aattaattgg gtattgaatt catgtaggca acaaaattga 1380
gggcctaata tttcctgtat aatgcaccaa aagggttctt acagaactga atgcctgaat 1440
agagagattc taggagattt ggtgaactag caactctgag ctctgttgtg ctgtattttc 1500
agagaatgtt ttttttgga gaacaggaat tgtactactt gtatttattg gaacttctac 1560
atcagtctgg atttgttcag aagaccttta gtgatttatg tatcagtga acttaaaaaa 1620
aaaaaaaaaa aa 1632

```

```

<210> 54
<211> 374
<212> PRT
<213> Oryza sativa

```

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<400> 54
Met Ala Val Pro Leu Val Leu Val Val Leu Pro Leu Gly Leu Leu Phe
  1              5              10              15

Leu Leu Ser Gly Leu Ile Ile Asn Ala Ile Gln Ala Val Leu Phe Leu
      20              25              30

Ser Ile Arg Pro Phe Ser Lys Ser Leu Tyr Arg Arg Ile Asn Arg Phe
      35              40              45

Leu Ala Glu Leu Leu Trp Leu Gln Leu Val Trp Leu Val Asp Trp Trp
      50              55              60

Ala Gly Val Lys Ile Gln Leu His Ala Asp Asp Glu Thr Tyr Lys Ala
      65              70              75              80

Met Gly Asn Glu His Ala Leu Val Ile Ser Asn Asn Arg Ser Asp Ile
      85              90              95

Asp Trp Leu Ile Gly Trp Ile Leu Ala Gln Arg Ser Gly Cys Leu Gly
      100             105             110

Ser Thr Leu Ala Val Met Lys Lys Ser Ser Lys Phe Leu Pro Val Ile
      115             120             125

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Gly	Trp	Ser	Met	Trp	Phe	Ala	Glu	Tyr	Leu	Phe	Leu	Glu	Arg	Ser	Trp
130						135					140				
Ala	Lys	Asp	Glu	Lys	Thr	Leu	Lys	Trp	Gly	Leu	Gln	Arg	Leu	Lys	Asp
145					150					155					160
Phe	Pro	Arg	Pro	Phe	Trp	Leu	Ala	Leu	Phe	Val	Glu	Gly	Thr	Arg	Phe
				165					170					175	
Thr	Pro	Ala	Lys	Leu	Leu	Ala	Ala	Gln	Glu	Tyr	Ala	Val	Ser	Gln	Gly
			180					185						190	
Leu	Pro	Ala	Pro	Arg	Asn	Val	Leu	Ile	Pro	Arg	Thr	Lys	Gly	Phe	Val
		195					200					205			
Ser	Ala	Val	Thr	Ile	Met	Arg	Asp	Phe	Val	Pro	Ala	Ile	Tyr	Asp	Thr
	210					215					220				
Thr	Val	Ile	Ile	Pro	Lys	Asp	Ser	Pro	Gln	Pro	Thr	Met	Leu	Arg	Ile
225					230					235					240
Leu	Lys	Gly	Gln	Ser	Ser	Val	Val	His	Val	Arg	Met	Lys	Arg	His	Ala
				245				250						255	
Met	Ser	Glu	Met	Pro	Lys	Ser	Glu	Asp	Asp	Val	Ser	Lys	Trp	Cys	Lys
			260					265					270		
Asp	Ile	Phe	Val	Ala	Lys	Asp	Ala	Leu	Leu	Asp	Lys	His	Leu	Ala	Thr
	275						280					285			
Gly	Thr	Phe	Asp	Glu	Glu	Ile	Arg	Pro	Ile	Gly	Arg	Pro	Val	Lys	Ser
	290					295					300				
Leu	Leu	Val	Thr	Leu	Phe	Trp	Ser	Cys	Leu	Leu	Leu	Tyr	Gly	Ala	Val
305					310					315					320
Lys	Leu	Phe	Leu	Trp	Thr	Gln	Leu	Leu	Ser	Thr	Trp	Lys	Gly	Val	Gly
				325					330					335	
Phe	Thr	Gly	Leu	Gly	Leu	Ala	Leu	Val	Thr	Ala	Val	Met	His	Val	Phe
			340					345					350		
Ile	Met	Phe	Ser	Gln	Ser	Glu	Arg	Ser	Ser	Ser	Ala	Lys	Ala	Ala	Arg
		355					360					365			
Asn	Arg	Val	Lys	Lys	Asp										
	370														

<210> 55  
 <211> 1498  
 <212> DNA  
 <213> Glycine max

<400>	55														
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tcgttgcggtt	gtgctctgct	ctgctccttt	gggcctgggc	tgggctgggc	tgggctgggc										120
tgggcatggc	tattgcagca	gcggccgtgg	tggtaccatt	gggcctgctc	ttcttcgcct										180
ccggcctcct	tgtaaatctc	attcaggcaa	tatgctatgt	cgtcgtaagg	ccggtgtcga										240
aaagtttgta	cagaaggatc	aaccgggtag	tagcagagct	cttgtggctg	gagcttgtat										300
ggcttattga	ttggtgggca	ggagttaagg	tccaaatatt	cacagatcat	gaaacctttc										360



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gtttaatggg taaagagcat gcacttgtga taagcaatca cagaagtgat attgattggc 420
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agaaatcttc aaagtttctg ccggtcattg gctgggtcaat gtgggttttct gagtatcttt 540
ttctggagag aagttgggccc aaggatgaaa gcacattaaa gtcaggcatc cagcgactga 600
gtgatttccc tcttcccttt tggctagctc tctttgtaga aggaacgcgt tttacacagg 660
ccaaactatt agctgctcag gaatatgcca cttccactgg attgcctggt cctagaaatg 720
ttttgattcc aagaactaag ggttttgttt ctgcagtaag tcatatgcgc tcatttggtc 780
ctgccattta tgatgtaaca gtagccatcc ctaagagttc ccctgctcct acaatgctaa 840
gactcttcaa gggacaacct tcagtgggtgc atgttcatat caagaggcat ttgatgaagg 900
aactgccaga tacagatgag gctgttgctc aatgggtgctg agatatattt gtggccaagg 960
atgctttgtt agacaaacat atggctgagg gtacttttag tgatcaagag ctgcaggata 1020
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ggctctgtaa gttcctgcaa tggctctcgt tactctcttc ctggaagggt gttgcatttt 1140
cagcttttgg tttggcagtt gttactgcac ttatgcaaat tctgattcaa ttctcacagt 1200
cagagcgttc aaacccggcc aagatcgtgc ctgcaaagtc aaaaaacaag gggctcttgat 1260
ttatttggcg aacttaaagt tgcatttatg tgtgatgagt gactcatgta atactcatta 1320
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atggcctaga aaaattcaac cacctatttt attttaaaaa aaaaaaaaaa aaaaaact 1498

```

```

<210> 56
<211> 377
<212> PRT
<213> Glycine max

```

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<400> 56
Met Ala Ile Ala Ala Ala Val Val Val Pro Leu Gly Leu Leu Phe
 1                5                10                15

Phe Ala Ser Gly Leu Leu Val Asn Leu Ile Gln Ala Ile Cys Tyr Val
      20                25                30

Val Val Arg Pro Val Ser Lys Ser Leu Tyr Arg Arg Ile Asn Arg Val
      35                40                45

Val Ala Glu Leu Leu Trp Leu Glu Leu Val Trp Leu Ile Asp Trp Trp
      50                55                60

Ala Gly Val Lys Val Gln Ile Phe Thr Asp His Glu Thr Phe Arg Leu
      65                70                75                80

Met Gly Lys Glu His Ala Leu Val Ile Ser Asn His Arg Ser Asp Ile
      85                90                95

Asp Trp Leu Val Gly Trp Val Ser Ala Gln Arg Ser Gly Cys Leu Gly
      100                105                110

Ser Thr Leu Ala Val Met Lys Lys Ser Ser Lys Phe Leu Pro Val Ile
      115                120                125

Gly Trp Ser Met Trp Phe Ser Glu Tyr Leu Phe Leu Glu Arg Ser Trp
      130                135                140

Ala Lys Asp Glu Ser Thr Leu Lys Ser Gly Ile Gln Arg Leu Ser Asp
      145                150                155                160

Phe Pro Leu Pro Phe Trp Leu Ala Leu Phe Val Glu Gly Thr Arg Phe
      165                170                175

```

Thr	Gln	Ala	Lys	Leu	Leu	Ala	Ala	Gln	Glu	Tyr	Ala	Thr	Ser	Thr	Gly	
			180					185					190			
Leu	Pro	Val	Pro	Arg	Asn	Val	Leu	Ile	Pro	Arg	Thr	Lys	Gly	Phe	Val	
		195					200					205				
Ser	Ala	Val	Ser	His	Met	Arg	Ser	Phe	Val	Pro	Ala	Ile	Tyr	Asp	Val	
	210					215					220					
Thr	Val	Ala	Ile	Pro	Lys	Ser	Ser	Pro	Ala	Pro	Thr	Met	Leu	Arg	Leu	
225					230					235					240	
Phe	Lys	Gly	Gln	Pro	Ser	Val	Val	His	Val	His	Ile	Lys	Arg	His	Leu	
				245					250					255		
Met	Lys	Glu	Leu	Pro	Asp	Thr	Asp	Glu	Ala	Val	Ala	Gln	Trp	Cys	Arg	
		260						265					270			
Asp	Ile	Phe	Val	Ala	Lys	Asp	Ala	Leu	Leu	Asp	Lys	His	Met	Ala	Glu	
	275						280					285				
Gly	Thr	Phe	Ser	Asp	Gln	Glu	Leu	Gln	Asp	Thr	Gly	Arg	Pro	Ile	Lys	
	290					295					300					
Ser	Leu	Leu	Val	Val	Ile	Ser	Trp	Ala	Cys	Leu	Val	Val	Ala	Gly	Ser	
305					310					315					320	
Val	Lys	Phe	Leu	Gln	Trp	Ser	Ser	Leu	Leu	Ser	Ser	Trp	Lys	Gly	Val	
				325					330					335		
Ala	Phe	Ser	Ala	Phe	Gly	Leu	Ala	Val	Val	Thr	Ala	Leu	Met	Gln	Ile	
			340					345					350			
Leu	Ile	Gln	Phe	Ser	Gln	Ser	Glu	Arg	Ser	Asn	Pro	Ala	Lys	Ile	Val	
	355						360					365				
Pro	Ala	Lys	Ser	Lys	Asn	Lys	Gly	Ser								
	370					375										

<210> 57  
 <211> 1415  
 <212> DNA  
 <213> Triticum aestivum

<400>	57																
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tcttgacgat	aaggccattc	tcgaagcgat	tgtaccggca	gatcaacgta	ttcctggccg												180
agttgttggtg	gcttcagctg	atctggcttg	tggactgggtg	ggcagggtatt	aagggtacagg												240
tgtatgcgga	tccagaaact	tggaaactaa	tgggcaaaga	gcacgccctt	ctcatatcca												300
atcatcgaag	tgacattgat	tggctgggtg	gatggatttt	agcacagcgt	tcaggatgtc												360
ttggaagcgc	aatagctata	atgaagaaat	cctcaaagtt	ccttccagtt	attgggttgg												420
ccatgtgggtt	tgcagaatac	ctcttttttg	agagaagctg	ggcaaaggat	gaaaaaacac												480
ttaaatcggg	tcttcaaagg	ttgaaagact	tccccagatc	atthttggctt	gccctttttg												540
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aggggtttgac	agcgcctagg	aatgtgctga	ttccacgaac	aaagggattt	gtatcagctg												660
taagtattat	gcgtgacttt	gtcccagcta	tctacgatac	aacagtgatt	attccggaag												720
attcgcctaa	accaacaatg	ctgcgtattc	ttcagggaca	atcatcagtt	gttcatgtcc												780
gcataaaaacg	ccattcaatg	agtgatatgc	ctaactcgga	tgaggatgtt	tcaaaatggt												840
gcaaagatat	atttgtagca	aaggacgcgt	tattggacaa	acatatagca	actgggtactt												900

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cgaagctttt ttttatcaaa aaaaaaaaaa aaaaa 1415

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```

<210> 58
<211> 374
<212> PRT
<213> Triticum aestivum

```

```

<400> 58
Met Ala Ile Pro Leu Val Leu Leu Pro Leu Gly Leu Leu Phe
 1          5          10          15

Leu Leu Ser Gly Leu Val Val Asn Thr Val Gln Ala Val Leu Phe Leu
          20          25          30

Thr Ile Arg Pro Phe Ser Lys Arg Leu Tyr Arg Gln Ile Asn Val Phe
          35          40          45

Leu Ala Glu Leu Leu Trp Leu Gln Leu Ile Trp Leu Val Asp Trp Trp
          50          55          60

Ala Gly Ile Lys Val Gln Val Tyr Ala Asp Pro Glu Thr Trp Lys Leu
          65          70          75          80

Met Gly Lys Glu His Ala Leu Leu Ile Ser Asn His Arg Ser Asp Ile
          85          90          95

Asp Trp Leu Val Gly Trp Ile Leu Ala Gln Arg Ser Gly Cys Leu Gly
          100          105          110

Ser Ala Ile Ala Ile Met Lys Lys Ser Ser Lys Phe Leu Pro Val Ile
          115          120          125

Gly Trp Ser Met Trp Phe Ala Glu Tyr Leu Phe Leu Glu Arg Ser Trp
          130          135          140

Ala Lys Asp Glu Lys Thr Leu Lys Ser Gly Leu Gln Arg Leu Lys Asp
          145          150          155          160

Phe Pro Arg Ser Phe Trp Leu Ala Leu Phe Val Glu Gly Thr Arg Phe
          165          170          175

Thr Pro Ala Lys Leu Leu Ala Ala Gln Glu Tyr Ala Val Ser Gln Gly
          180          185          190

Leu Thr Ala Pro Arg Asn Val Leu Ile Pro Arg Thr Lys Gly Phe Val
          195          200          205

Ser Ala Val Ser Ile Met Arg Asp Phe Val Pro Ala Ile Tyr Asp Thr
          210          215          220

Thr Val Ile Ile Pro Glu Asp Ser Pro Lys Pro Thr Met Leu Arg Ile
          225          230          235          240

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Leu	Gln	Gly	Gln	Ser	Ser	Val	Val	His	Val	Arg	Ile	Lys	Arg	His	Ser			
				245					250					255				
Met	Ser	Asp	Met	Pro	Asn	Ser	Asp	Glu	Asp	Val	Ser	Lys	Trp	Cys	Lys			
			260					265					270					
Asp	Ile	Phe	Val	Ala	Lys	Asp	Ala	Leu	Leu	Asp	Lys	His	Ile	Ala	Thr			
		275					280					285						
Gly	Thr	Phe	Asp	Glu	Glu	Ile	Ile	Pro	Ile	Gly	Arg	Pro	Val	Lys	Ser			
	290					295					300							
Leu	Met	Val	Val	Leu	Ser	Trp	Ser	Cys	Leu	Leu	Leu	Tyr	Gly	Ala	His			
305					310					315					320			
Arg	Phe	Leu	Gln	Trp	Thr	Gln	Leu	Leu	Ser	Thr	Trp	Lys	Gly	Val	Ile			
				325					330					335				
Leu	Phe	Ala	Ser	Gly	Leu	Ala	Met	Val	Thr	Ala	Val	Met	His	Val	Phe			
			340					345					350					
Ile	Met	Phe	Ser	Gln	Ala	Glu	Arg	Ser	Ser	Ser	Ala	Lys	Ala	Ala	Arg			
		355					360					365						
Asp	Arg	Val	Lys	Lys	Asp													
		370																